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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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length: 2000000000
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AAB11832
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AAY40901
AAB73254
AAY40905
AAU02882
AAY40902
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                                                                                                                                                                                                                                                                                                                                                                           distribution.
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melanog
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151.5	159.5	159.5	172.5	197.5	197.5	202	226.5	236	251.5	255	255	256.5	269.5	289	290	290	299	299	310.5	348	354	423	445	451	457.5	461	483	537.5	537.5	556	568	575.5	595
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AAY36089	AAG91332	AAB76843	AAM24336	AAU37141	AAU34281	AAB96555	ABG10933	ABB52506	AAU35119	AAM23744	AAM23715	AAY40903	ABG10934	AAY40907	ABG29884	AAU01581	AAB90591	AAB90590	AAM24062	AAU01608	AAU01607	AAU02884	AAY40906	AAU02883	AAR44143	AAW11325	ABB58504	AAB90637	AAB90555	AAY44016	AAY44017	ABB65651	96
Extended human sec	C glutamicum prote	Corynebacterium gl	Drosophila EST enc		Staphylococcus aur	Putative P. abyssi	Novel human d‰agno	Escherichia coli p	Enterococcus faeca	enc	Human EST encoded	Arabidopsis thalia	Novel human diagno	Arabidopsis thalia	Novel human diagno	Human secreted pro	secreted	Human secreted pro		Human secreted pro	Gene #21 human sec			Human HsNHE-6 poly	Rabbit sodium ion/	Human Na+/H+ excha	Drosophila melanog		Human secreted pro	Schizosaccharomyce	Saccharomyces cere	Drosophila melanog	Cat flea HMT Na/H

ALIGNMENTS

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Morning glory-originated gene encoding a protein with pH regulation activity in vacuoles, useful in controlling flower color to give new breeds of colorful plants for cut flowers, particularly applicable in horticulture -
                                                        WPI; 2001-191648/19.
N-PSDB; AAF75752.
                                                                                    Iída S,
                                                                                                                           24-AUG-1999;
                                                                                                                                             24-AUG-2000; 2000WO-JP05722.
                                                                                                                                                                01-MAR-2001.
                                                                                                                                                                                   WO200114560-A1
                                                                                                                                                                                                                         Vacuole pH regulation; morning glory; flower colour.
                                                                                                                                                                                                                                           Protein regulating the pH of vacuoles
                                                                                                                                                                                                                                                               14-MAY-2001
                                                                                                                                                                                                                                                                                  AAB73251;
                                                                                                                                                                                                                                                                                                     AAB73251 standard; Protein; 542
                                                                                                        (SUNR ) SUNTORY LTD.
                                                                                                                                                                                                       Ipomoea nil.
                                                                                    Tanaka S,
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                                                                                                                           99JP-0236800.
                                                                                    Inagaki
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RESULT 2
AAB12786
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Best Local :
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            JP2000157287-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a protein from Morning Glory, which has vacuola pH regulatory activities. The protein enables flower colour to be controlled via regulation of the vacuolar pH, colours can range from bl to red in colour spectrum. The protein is useful in controlling flower colour to give new breeds of colourful plants for cut flowers, particularly applicable in horticulture.
                                Atliplex gmelini
                                                                                      Atliplex gmelini
                                                                 Atliplex
                                                                                                            23-NOV-2000
                                                                                                                                   AAB12786
                                                                                                                                                      AAB12786 standard;
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                                                                                                                                                                                                                                 PR 542
                                                                                                                                                                                                                                                               ESDMITGPEVARPTALRMLLRTPTHTVHRYWRKFDDSFMRPVFGGRGFVPFVAGSPVEQS
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                                                      x gmelini;
H+ antipor
                                                                                                                                                                                                            542
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                                                      antiporter
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                                                                                                           (first
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                                                                                   Na+ and H+ antiporter protein.
                                                                Na
                                                                                                                                                      Protein;
                                                                                                           entry)
                                                   plus and H plus antiporter protein; protein; transformed plant; high s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 2768; DB 22;
Pred. No. 4.8e-270;
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                                                     tolerance
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RESULT 3
AAB73253
ID AAB7
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AC AAB7
XX

AAB73253

standard;

Protein;

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Best Local Simi
Matches 418;
                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents an Na+ and H+ antiporter protein isolated from Atliplex gmelini. The Na+ and H+ antiporter protein and gene encoding it are useful for the preparation of transformed plants with high salt tolerance, e.g. for growth in arid land.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure;
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                                 482
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                                                                                                                                                                    LSSLLQN--SDLFTSDHASYVSMNLFVALLCACIVLGHLLEENRWVNESITALIIGLCTG
                                                                         VTVVLFSTVVFGLMTKPLINLLLPPHKQMPSGHSSMTTSEPSSPKHFTVPLLDNQPDSES
                                                                                                  HSFATLSFVAETFIFLYVGMDALDIEKWKFVKNSQGLSVAVSSILVGLILVGRAAFVFPL
                                                                                                                                                                                                                                      SPVEQS
                                                                  ISVVLFSTMVFGLLTKPLIMFLLPQPKHFT--
SPTEQS
                                DVGNGNHEDTTEPRTIVRPSSLRMLLNAPTHTVHHYWRKFDDSFMRPVFGGRGFVPFVPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Page 10-12;
                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      plus antiporter protein and
                                                                                                                                                                                                                                                                                                                                                                            AA;
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                                                 -VARPTALRMLLRTPTHTVHRYWRKFDDSFMRPVFGGRGFVPFVAG
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76.6%;
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Pred. No. 1.8e-205;
0; Mismatches 65;
                                                                 - SCSTVSDVGSPKSYSLPLLEGNQDYEV
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14-MAY-2001

(first entry)

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                                                                                                  TTRHSFATLSFVAETFIFLYVGMDALDIEKWKFVKNSQGLSVAVSSILVGLILVGRAAFV
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                                                  FPLSFLSNLAKKNSSDKISFRQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMI
                                                                                     TTKHTFATLSFIAEIFIFLYVGMDALDIEKWKFVSDSPGTSIKVSSILLGLVLVGRGAFV
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)B; AAF75765.
                                     FPLSFLSNLTKKNPEDKISFNQQVTIWWAGLMRGAVSMALAYNQFTRGGHTQLRANAIMI
                                                                                                                                                                                                             FGEGVVNDATSVVLFNAIQSFDMTSFDPKIGLHFIGNFLYLFLSSTFLGVGIGLLCAYII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Morning glory-originated gene encoding a protein with pH regulation activity in vacuoles, useful in controlling flower color to give new breeds of colorful plants for cut flowers, particularly applicable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vacuole pH regulation; flower colour
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                                                    FGEGVVNDATSVVLFNAIQNFDLSHIDTGKAMELVGNFLYLFASSTALGVAAGLLSAYII
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412; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 2103.5; DB 2;
Pred. No. 4.7e-203;
1; Mismatches 69;
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                                                                                                        Query Match
Best Local S
Matches 401
                                                                                                                                                                                                          This sequence represents a novel rice Na+/H+ antiporter (countertransporter), OSNHX1. The invention relates to OSNHX1 and nucleic acids which encode it; vectors, host cells and transgenic; containing OSNHX1 nucleic acids; recombinant expression of OSNHX1; antibodies which recognise OSNHX1. OSNHX1 nucleic acids are useful production of salt tolerant transgenic plants.
                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                          DNA encoding a sodium ion and rice origin for production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OsNHX1; Na+/H+ antiporter; sodium/proton antiporter; countertransporter; active transport; rice; transgenic plant; salt-tolerance.
                                                                                                                                                                                                                                                                                                                                       Claim la; Fig 1; 43pp; Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fukuda A,
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DB; AAA61876.
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                                                                                                          401;
                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tanaka Y;
                                                                                                                                                                                535
                                                                                                          Conservative
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                                                                                                       74.3%; Score 2055.5; DB 21; Length 76.4%; Pred. No. 3.2e-198; tive 49; Mismatches 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                535
                                                                                                                                                                                                                                                                                                                                                                            proton counter-transporter protein salt tolerant rice transformants
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                                                                                                       Gaps
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                                                                                                                                                                                                                                                (BLUM/)
                               Claim 36; Fig 1A;
                                                                  Nucleic acid molecules encoding sodium/proton transport polypeptides, useful in genetic engineering salt tolerance in crop plants
                                                                                                                         N-PSDB; AAZ22591.
                                                                                                                                           WPI; 1999-571840/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sodium; proton; antiport; transporter; salt tolerance; salt management; transgenic plant; survival; soil; farming; accumulation; irrigation;.
The invention relates to an isolated nucleic acid molecule encoding
                                                                                                                                                                            Blumwald E, Apse M,
                                                                                                                                                                                                                                                                                                      18-MAR-1998;
15-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                         18-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                              23-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
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                                                                                                                                                                                                                 (AHAR/)
                                                                                                                                                                                                                                    (SNED/)
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                                                                                                                                                                                                               SNEDDEN W. AHARON G.
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99US-0116111.
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                               93pp;
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                                  English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 399
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                                                  14-MAY-2001
Vacuole pH regulation; flower
                        Protein regulating the pH of vacuoles
                                                                                                   AAB73254 standard;
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                                                                                                                                                                                                                   FIEPSGNHNVPRPDSIRGFLTRPTRTVHXYWRQFDDSFMRPVFGGRGFVPFVPGSPTERN
                                                                                                                                                                                                                                  TFATLSFLAETFIFLYVGMDALDIDKWRSVSDTPGTSIAVSSILMGLVMVGRAAFVFPLS
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                                                 entry)
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; pred. No. 9.3e-197;
57; Mismatches 71;
 colour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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Best Local S
Matches 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a protein, which has vacuolar pH regulatory activities. The protein enables flower colour to be controlled via regulation of the vacuolar pH, colours can range from blue to red in colour spectrum. The protein is useful in controlling flower colour to give new breeds of colourful plants for cut flowers, particularly .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morning glory-originated gene encoding a protein with pH regulation activity in vacuoles, useful in controlling flower color to give ne breeds of colorful plants for cut flowers, particularly applicable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SUNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            applicable in horticulture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 7; Page 57-60; 68pp; Japanese
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DB; AAF75766.
                                                                                                                                                                                                                                                                                                                                                             GFESVIKLAASETDNLWSSGHGSVVAITLFVTLLCTCIVIGHLLEENRWMNESIIALIIG
                                                                                                                                                                                                                                        VFGEGVVNDATSVVLFNAIQSFDMTSFDPKIGLHFIGNFLYLFLSSTFLGVGIGLLCAYI
                                                                                                                                                                                                                                                                                   GTLISCSIISFGAVKIFKHLDIDFLDFGDYLAIGAIFAATDSVCTLQVLSQDETPLLYSL
                                                                                                                                GTLISFIIISLGTIAFFPKMNMR-LGVGDYLAIGAIFAATDSVCTLQVLSQDETPLLYSL
                                                                                                 VFPLSFLSNLAKKNSSDKISFRQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENAIM
                                                                                                                                                                                                                          VFGEGVVNDATSVVLFNAVQNFDLPHMSTAKAFELVGNFFYLFATSTVLGVLTGLLSAYI
                                                                                                                                                                                                                                                                                                                                                                                                           389;
DSVAELFSIRGOTSQGGEPVARPSSLRMLLTKPTHTVHYYWRKFDNAFMRPVFGGRGFVP
                     DSESDMIT-----
                                                   | ITSTVTVVLFSTVVFGLMTKPLINLLLPPHKQMPSGHSSMTTSEPSSPKHFTVPLLDNQP
                                                                                      VFPLSFLSNLAKKSPLEKISLRQQIIIWWAGLMRGAVSMALAYKQFTREGLTVERENAIF
                                           ITSTITIVLESTVVFGLMTKPLINLLIPSPKLNRS-----VSSEPLTPNSITIPLLGESQ
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                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 70.5
89; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       555 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                      70.6%;
70.5%;
          -GPEVARPTALRMLLRTPTHTVHRYWRKFDDSEMRPVFGGRGFVP
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                                                                                                                                                                                                                                                                                                                                                                                                          Score 1953.5; D
Pred. No. 6.4e-1
56; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       DB 2
-188;
88;
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                                                                                          Query Match
Best Local
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                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid molecule encoding a plant Na/H antiport (PNHX) transporter polypeptide, or a fragment and capable of increasing salt tolerance in a cell. This sequence corresponds to a transporter from Arabidopsis thaliana. The Na/H transporter polypeptides provide a means of intracellular salt management, particularly in plants. The sequences are useful for producing transgenic plants that are capable of surviving in soil with high salt levels that would normally inhibit growth of the crop species. This would be useful in farming land in areas that are generally considered unproductive through salt accumulation and poor irrigation,
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI;
    64
                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid molecules encoding sodium/proton transport polypeptides, useful in genetic engineering salt tolerance in crop plants - \,
                                                                                                                                 Sequence
                                                                                                                                                                       atriplex,
                                                                                                                                                                                  strawberries, spinach,
                                                                                                                                                                                                                                                                                                                                                                 Claim 50; Fig 5A-B; 93pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blumwald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-MAR-1998;
15-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        crop.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09947679-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY40905 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (AHAR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana Na/H transporter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY40905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SNED/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (APSE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BLUM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         531
                             N
VILLLSGGKSSHLLVFSEDLFFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTLIS
                                       LSSLLQN-SDLFTSDHASVVSMNLFVALLCACIVLGHLLEENRWVNESITALIIGLCTGV
                                                                                                                                                                                                           in India,
                                                                                                                                                                                                                                                                                                                                                                                                                                             1999-571840/48
                         LDSLVSKLPSLSTSDHASVVALNLFVALLCACIVLGHLLEENRWMNESITALLIGLGTGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FVAGSPVEQSPR 542
:| ||| |:| |
YVPGSPTERSVR 547
                                                                            al Similarity
369; Conserv
                                                                                                                                                                            n India, Australia, and prairies in USA or Canada. Commer
such as potatoes, tomatoes, brassica, cotton, sunflower,
erries, spinach, lettuce, rice, soybean, corn, wheat, rye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNEDDEN W. AHARON G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BLUMWALD E.
                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ22595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proton; antiport; transporter; salt tolerance; salt management;
nic plant; survival; soil; farming; accumulation; irrigation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APSE M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'n
                                                                                                                                                       sorghum, alfalf salt tolerance.
                                                                                                                                 547
                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apse M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98US-0078474.
99US-0116111.
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                                                                                                                                                                   alfalfa, salicornia and others would benefit from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                       67.4%;
73.2%;
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                                                                                                                                                                                                                                                                                                                                                                 English.
                                                                              54;
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                                                                                       Score 1867;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Σ
                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aharon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                farming; accumulation; irrigation;
                                                                           ; DB 20;
3.3e-179;
hes 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G;
                                                                           Indels
                                                                                                     Length 547;
                                                                           14;
                                                                                                                                                                               rye,
                                                                        Gaps
                                                                                                                                                                              barley,
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RESULT 9
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18-AUG-2000;
22-AUG-2000;
                                                                                    WPI; 2001-328862/34.
                                                                                                          Gaiola
                                                                                                                                                                                                                                                                                            freeze tolerance; 35S promoter; sodium; calcium; manganese; saline soil; thale-cress.
                                                                                                                                                                                                                                                                                                               AtNHX1; tonoplast pyrophosphatase hydrogen ion translocating pump; AV vacuolar pyrophosphatase; salt tolerance; drought tolerance; cation;
                                                                                                                             (WYCO-) UNIV CONNECTICUT (WHED ) WHITEHEAD INST.
                                                                                                                                                                                                        10-NOV-2000; 2000WO-US30955
                                                                                                                                                                                                                              17-MAY-2001
                                                                                                                                                                                                                                                   WO200133945-A1
                                                                                                                                                                                                                                                                        Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana AtNHX1 polypeptide
                                                                                                                                                                                                                                                                                                                                                                       12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                            AAU02882;
                                                                                                                                                                                                                                                                                                                                                                                                                 AAU02882 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLSNLAKKNSSDKISFRQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMITSTV 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SFATLSFVAETFIFLYVGMDALDIEKWKFVKNSQGLSVAVSSILVGLILVGRAAFVFPLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FGRHSTDREVALMMLMSYLSYIMAELFYLSGILTVFFCGIVMSHYTWHNVTESSRVTTRH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TFATLSFLAETFIFLYVGMDALDIDKWRSVSDTPGTSIAVSSILMGLVMVGRAAFVFPLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | CSIISFGAVKIFKHLDIDFLDFGDYLAIGAIFAATDSVCTLQVLSQDETPLLYSLVFGEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLSNLAKKNQSEKINFNMQVVIWWSGLMRGAVSMALAYNKFTRAGHTDVRGNAIMITSTI
                                                                                                          RA;
                                                                                                                                                             ; 99US-0164808.
; 2000US-0226223.
; 2000US-0644039.
                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
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                                                                                                                                                                                                                                                                                                                           AVP1;
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The sequence represents an Arabidopsis thaliana AtNHX1 polypeptide which

Transgenic plants with salt tolerance, and increased yield and flower size con

vacuolar pyrophosphatase

expression comprise

drought and freeze

resistance genes or

Example 1; Fig

6;

68pp; English

increased

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RESULT 10
AAY40902
ID AAY40
XX
AC AAY40
XX
AC AAY40
XX
XX
DT 18-JA
XX
XX
XX
KW Sodiu
KW trans
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               is a tonoplast pyrophosphatase hydrogen ion (H+) translocating pump. Transgenic plants can be made by transforming plant cells with exogenous tonoplast pyrophosphate driven H+ pump genes and an exogenous nucleic acid encoding a protein, such as AVP1, which alters expression of vacuolar pyrophosphatase. Salt tolerance may be introduced into a plant via transformation of the cells to induce upregulation of vacuolar phosphashase expression. Drought and/or freeze tolerance may also be introduced through transformation with DNA encoding a vacuolar H+ translocating pump linked to a promoter such as the 35s promoter. These processes are useful for bioremediating soil and removing cations such as sodium, calcium, manganese and lead from soil or water which can support plant growth. Plants which grow in saline soil can be produced and yield and flower size of plants can be increased.
    Sodium; proton;
transgenic plan
                   Sodium;
                                             Arabidopsis thaliana Na/H transporter AtNHX2.
                                                                                18-JAN-2000
                                                                                                                                           AAY40902 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                       P 532
                                                                                                                                                                                                                                                                            FIEPSCNHNVPRPDSIRGFLTRPTRTVHYYWRQFDDSFMRPVFCCRGFVPFVPGSPTERN
                                                                                                                                                                                                                                                                                                                                                                                                                                                               P 541
                                                                                                                                                                                                                                                                                              ESDMITGPEVARPTALRMLLRTPTHTVHRYWRKFDDSFMRPVFGGRGFVPFVAGSPVEQS
                                                                                                                                                                                                                                                                                                                                        TVVLFSTVVFGLMTKPLINLLLPPHKQMPSGHSSMTT---
                                                                                                                                                                                                                                                                                                                                                                                                    FLSNLAKKNQSRKINFNMQVVIWWSGLMRCAVSMALAYNKFTRAGHTDVRGNAIMITSTI
                                                                                                                                                                                                                                                                                                                                                                                                                    FLSNLAKKNSSDKISFRQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMITSTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVNDATSVVLFNAIQSEDMISFDPKIGLHFIGNFLYLFLSSTFLGVGIGLLCAYIIKKLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDSLVSKLPSLSTSDHASVVALNLPVALLCACIVLGHLLSSNRWMNKSITALLIGLGTGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
pton; antiport; transporter; salt
plant; survival; soil; farming;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            571 AA;
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                                                                             (first
                                                                            entry)
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salt tolerance; sa
ing; accumulation;
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              salt management;
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                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                              The Na/H transporter polypeptides provide a means of intracellular salt management, particularly in plants. The sequences are useful for producing transgenic plants that are capable of surviving in soil with high salt levels that would normally inhibit growth of the crop species. This would be useful in farming land in areas that are generally considered unproductive through salt accumulation and poor irrigation, e.g. in India, Australia, and prairies in USA or Canada. Commercial crops, such as potatoes, tomatoes, brassica, cotton, sunflower, strawberries, spinach, lettuce, rice, soybean, corn, wheat, rye, barley atriplex, sorghum, alfalfa, salicornia and others would benefit from
                                                                                                                                                                                                                                                                                                                                                                                                                 strawberries, spinach, lettuce, rice, s
atriplex, sorghum, alfalfa, salicornia
increased salt tolerance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid molecule encoding a plant Na/H antiport (PNHX) transporter polypeptide, or a fragment and capable of increasing salt tolerance in a cell. This sequence corresponds to the AtNHX2 transporter from Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid molecules encoding sodium/proton transport polypeptides, useful in genetic engineering salt tolerance in crop plants .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-571840/48
N-PSDB; AAZ22592.
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15-JAN-1999;
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299
                          301
                                                                                                             179
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(APSE/) APSE M.
(SNED/) SNEDDEN W.
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                                                                                                                                                                                                                                                                                          TRHSFATLSEVAETFIFLYVGMDALDIEKWKFVKNSQGLSVAVSSILVGLILVGRAAFVF
                                                 GEGVVNDATSVVLENAIQSEDMTSFDPKIGLHFIGNFLYLFLSSTFLGVGIGLLCAYIIK 240
                                                                                                                                                                 LISCSIISFGAVKIFKHLDIDFLDFGDYLAIGAIFAATDSVCTLQVLSQDETPLLYSLVF 180
                                                                                                                                                                                                                                  TGVVILLLSGGKSSHLLVESEDLEFIYLLPPIIFNAGFQVKKKQFEVNEMTIMLFGAIGT 120
                                                                                                                                                                                                                                                                           ## HSIGLTEEVTNK--LAAEHPQVIPISVFIAILCLCLVIGHLLEENRWVNESITAILVGAA 58
SRHVFAMLSFIAETFIFLYVGTDALDFTKWKTSSLSFGGTLGVSGVITALVLLGRAAFVF
                                                                                                         GEGVVNDATSVVLFNAVQKIQFESLTGWTALQVFGNFLYLFSTSTLLGIGVGLITSFVLK
                                                                                                                                                                                                                     SGTVILLISKGKSSHILVFDEELFFIYLLPPIIFNAGFQVKKKKFFHNFLTIMSFGVIGV 118
                                                                                                                                                                                                                                                                                                                                     310;
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AHARON G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93pp;
                                                                                                                                                                                                                                                                                                                                                57.8%; Score 1599.5; DB 20; 58.7%; Pred. No. 2.9e-152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Snedden
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                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 4884; 21pp + Sequence Listing; English
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N-PSDB; ABL03467.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ITSTVTVVLFSTVVFGLMTKPLINLLLPPHKQMPSGHSSMTTSEPSSPKH-FTVPLLDNQ
STLVTDPPLIDSHAVEQEHNSSLSLFFVICVIMLGILLIHSMLQTGFQYLPESIVVVFLG
                                            SSLLQNSDLFTS-----DHASVVSMNLFVALLCACIVLGHLLEEN--RWVNESITALIIG 58
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                                                                                                                Similarity
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No. 2.
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RESULT 12
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Cat
                                                                                                         Flea Malpighian tubule and head and nerve cord tissue derived nucleic acids useful for the prevention, diagnosis and treatment of flea
                                                                                                                                                                                                                                                                                                                      Cat flea; hindgut and Malpighian tubule protein; flea infestation; vaccine; antiparasitic; therap
                                                                                                                                                                                                                                                                                                                                                                                        AAB29621;
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                                                                                                                                                                                                                                                                                        Ctenocephalides
                                                                                                                                                                                                                                                                                                           diagnosis; detection.
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                                                                             Claim 10; Page 891-893; 964pp; English.
                                                                                                                                                                     Brandt KS,
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The invention relates to novel cat flea (Ctenocephalides felis) nucleicids which are expressed in hindgut and Malpighian tubule (HMT) tion or head and nerve cord (HMC) tissue. The invention also relates to

nucleic

the

encoded proteins. The invention additionally encompasses expression constructs, recombinant viruses and recombinant cells comprising the nucleic acids of the invention, recombinant production of the protein antibodies against the proteins, a method of identifying inhibitors of the proteins.

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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 173; Conserv
                   ABB65651
                                            ABB65651 standard; Protein;
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                                                                                                                                                                       -DDSFMRPVFGGR 526
                                                                                                                                                                                                                                    EPSSPKHETVPLL~--DNQPDSE--SDMITGPEVARPTALRMLLRTPTHTVHRYWRKF--
                                                                                                                                                                                                                                                                                                                                         --LCLIGRAANIFPLSWLVNQFREH---KITKKMAFIMWFSGL-RGAISYAL-----
                                                                                                                                                                                                                                                                                                                                                                                                             YTHENLSTYTQITMQQTMRTLAFIAETCVFAYLGMAIFSF----RHRVEPALVIWSIV
                                                                                                                                                                                                                                                                                                                                                                                                                                          YTWHNVTESSRVTTRHSFATLSFVAETFIFLYVGMDALDIEKWKFVKNSQGLSVAVSSIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVVFALISALLLKHVDLRKYPS-LELGMMLVFTYAPYVLAEGIHLSGIMAILFCGIVMSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VFAIFGTAISAFVVGAG-VYLLGMADVAYNLSFVESFAFGSLISAVDPVATVAIFHALDV
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%; Pred. No. 6.6e-51;
114; Mismatches 190
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Best Local :
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The sequence data for this patent did not form specification, but was obtained in electronic f at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic a
                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 23745; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Venter JC, Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAR-2000;
11-JUL-2000;
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                                                                                                    LSSLLQNSDLFTSDHASVVSMNLFVALLCACIVLGHLLEENR--WVNESITALIIGLCTG 62
MIGAAMGCLTA-LMTKFTRVRDFPLLESALFVLMSYSTFLLAEATELTGVVAVLFCGICQ 410
                FLGVGIGLLCAYIIKKLYFGRHSTDREVALMMLMSYLSYIMAELFYLSGILTVFFCGIVM 285
                                                                    YSLVFGEGVVNDATSVVLFNAIQS------
                                                                                                                                                                                                             AIIRY--AGTSATLVHMQVEPQGVPTYSDKLPPDTLWFRYPVNQTNGTKPPEGIKTYAYV 177
                                                                                                                                                                                                                                                                 LNHRIQSLDLL------VFVFLLALTVLTIMLFKHHRVSWLHETGLAVIYGLIVG 119
                                                    YALVLGESVLNDAVAIVLSGAIQNYGEHYSNTGEFETTAF-
                                                                                                                                                        FRGQVHDVDENEIDLKATFDPEVFFNIILPPIIFYAGYSLKKKYFFRNLGAILTFAIVGT 237
                                                                                                                                                                        Similarity
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2000US-0614150.
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                                                                                                                                                                                                                                                                                                                   20.8%; Score 575.5; DB 2
28.8%; Pred. No. 7.9e-49;
tive 99; Mismatches 196
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                                                                 ---FDMTSFDPKIGLHFIGNFLYLFLSST 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BLUM/) BLUMWALD E.
(APSE/) APSE M.
(SNED/) SNEDDEN W.
(AHAR/) AHARON G.
                                                                          The invention relates to an isolated nucleic acid molecule encoding a plant Na/H antiport (PNHX) transporter polypeptide, or a fragment and capable of increasing salt tolerance in a cell. This sequence corresponds to an Na/H antiport transporter from the budding yeast saccharomyces cerevisiae. The Na/H transporter polypeptides provide a means of intracellular salt management, particularly in plants. The sequences are useful for producing transgenic plants that are capable of surviving in soil with high salt levels that would normally inhibit growth of the crop species. This would be useful in farming land in areas that are generally considered unproductive through salt accumulation and
                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid molecules encoding useful in genetic engineering sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae Na/H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY44017 standard;
                              poor irrigation, e.g. in India, Aus
Commercial crops, such as potatoes,
                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 8B; 93pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Blumwald E,
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15-JAN-1999;
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     strawberries,
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99US-0116111
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t; survival;
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     spinach,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transporter;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            soil;
                                                                                                                                                                                                                                                                                                                                                                                                                                salt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ξ
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                                                                                                                                                                                                                                                                                                                                                                                                                             sodium/proton transport polypeptides,
alt tolerance in crop plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
                              Australia, and prairies in USA or Canada
bes, tomatoes, brassica, cotton,
        lettuce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aharon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         farming;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>ن</u>
     rice,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            accumulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  salt management;
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RESULT 15
AAY44016
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                Schizosaccharomyces
                                                                                                    Sodium;
                                                                                                                          Schizosaccharomyces pombe Na/H antiport transporter
                                                                                                                                                    18-JAN-2000
                                                                                                                                                                             AAY44016;
                                                                                                                                                                                                     AAY44016
                                                                                     transgenic
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                                                                                                                                                                                                                                                                                                                    AVSSNKNLPNNISTTGGNTFGGLNETENTSPNPARSSMDKRNLRDKLGTIFNSDSQWFQN 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIGVLIGILVALLLKHTHIRRY-PQIESCLILLIAYESYFFSNGCHMSGIVSLLFCGITL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MLSILIFAIPGTFISAVVIGI-ILYIWTFLGLESIDISFADAMSVGATLSATDPVTILSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLPSPDLPGSDDPIAGDPDVDLNPVTEEMFSSWALFIMLLLLISALWSSYYLTQKRIRAV 89
                                                                                                                                                                                                                                                                                             FDDSFMRPVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MRGAVSIALAYN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FLGVGIGLLCAYIIKKLYFGRHSTDREVALMMLMSYLSYIMAELFYLSGILTVFFCGIVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSQDET-PLLYSLVFGEGVVNDATSVVLFNAIQSFDMTSFDPKIGLHFIGNFLYLFLSST 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FMTIMLFGAIGTLISCSIISFGAVKIFKHLDIDFLD--FGDYLAIGAIFAATDSVCTLQV 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HETYLSIFYGMVIGLIIRMSPGHYIQDTYTFNSSYFFNYLLPPIILNSGYELNQVNFFNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLQNSDLFTSDHASV----VSMN------LFVALLCACIVLG---HLLEEN-RWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILVGLILVGRAAFVFPLS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KHYAYYNMSRRSQITIKYIFQLLARLSENFIFIYLGLELFTEVELVY----KPLLIIVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHYTWHNVTESSRVTTRHSFATLSFVAETFIFLYVGMDALDIEKWKFVKNSQGLSVAVSS
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                                                                                                                                                                                                                                                                     FDEQVLKPVF
                                                                                                                                                                                                                                                                                                                                                                      IKTGCISEEDTSDDEFDIEAPRAINLLNGSSIQTDLGPYSD------NNSPDISIDQF
                                                                                                                                                                                                                                                                                                                                                                                                                         -RGAVGVALALGIQGEYKFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I---SICVARWCAVFPLSQFVNWIYRVKTIRSMSGITGENISVPDEIPYNYQMMTFWAGL
                                                                                    proton; antiport; transporter;
nic plant; survival; soil; farmi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 27.2
56; Conservative
                                                                                                                                                                                                      standard; Protein;
                                                                                                                                                    (first entry
                                                                                                                                                                                                                                                                     909
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                                                 pombe
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Pred. No. 3.7e
17; Mismatches
                                                                                                                                                                                                      569
                                                                                                                                                                                                                                                                                                                                                TGPEVARPTALRMLLRTPTHTV----HRYWRK 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---FLSNLAKKNSS--DKISFRQQIIIWWAGL
                                                                                      farming; accumulation;
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                                                                                                    salt
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3.7e-48;
hes 203;
                                                                                                    tolerance;
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                                                                                                    salt management;
                                                                                      irrigation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid molecule encoding CC a plant Na/H antiport (PNHX) transporter polypeptide, or a fragment CC and capable of increasing salt tolerance in a cell. This sequence CC corresponds to an Na/H antiport transporter from the fission yeast CC schizosaccharomyces pombe. The Na/H transporter polypeptides provide CC a means of intracellular salt management, particularly in plants. The CC sequences are useful for producing transgenic plants that are capable CC of surviving in soil with high salt levels that would normally inhibit CC growth of the crop species. This would be useful in farming land in areas CC that are generally considered unproductive through salt accumulation and CC commercial crops, such as potatoes, tomatoes, brassica, cotton, CC sunflower, strawberries, spinach, lettuce, rice, soybean, corn, wheat, CC rye, barley, atriplex, sorghum, alfalfa, salicornia and others would cC benefit from increased salt tolerance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 162; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid molecules encoding sodium/proton transport polypeptides useful in genetic engineering salt tolerance in crop plants - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-MAR-1998;
15-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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(APSE/) APSE M.
(SNED/) SNEDDEN W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-MAR-1999;
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    422
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                                       418 MITSTVTVVLFSTVVFGLMTKPLINLL----------LPPHKQMPS---GHSS 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 SMNLFVALLCACIVLGHLL------EENRWVNESITALIIGLCTGVVILLLSGGKSSHL 76
                                                                                                                                                                                                                                                                                                                                                                                       SFLNFENLSMTFVEALSMGATLSATDPVTVLAIFNSYKVDQKLYTIFGESTLNDAVAIV 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSFHSTYFFNVLLPPIILNSGYELHQSNFFRNIGTILTFAFAGTFISA--VTLGVLVYIF 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVESEDLEFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTLISCSIISFGA-VKIF 135
                                                                                                                                                                                                                                                                                                                                                LFNAIQSFDMTSFDPKIGLHF-----IGNFLYLFLSSTFLGVGIGLLCAYIIKKLYFGR 246
                                                                                                                                                                                                                                                                                                                                                                                                                            KHLDIDFLD--FGDYLAIGAIFAATDSVCTLQVL-SQDETPLLYSLVFGEGVVNDATSVV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWALFILLV----LLIGALLTSYYVQSKKIRAIHETVISVFVGMVVGLIIRVSPGLIIQNM
                                                                                                                                                                                                                                YPS-IESCIILLMAYTSYFFSNGCHMSGYVSLLFCGITLKHYAFFNMSYKAKLSTKYVFR 321
LRATTLYVVVLTLIIFGGTTARMLEILHIETGVAADVDSDTEIGMLPWQQSPEFDLENSA
                                                                                                SFLSNLAKK----NSSDKISFRQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENA-I 417
                                                                                                                                                        VLAQLSENFIFIYLGMSLFTQVDLVYKPIFILIT---TVAVTA-----SRYMNVFPL 370
                                                                                                                                                                                           TLSFVAETFIFLYVGMDALD----IEKWKFVKNSQGLSVAVSSILVGLILVGRAAFVFPL 362
                                                                                                                                                                                                                                                                     HSTDREVALMMLMSYLSYIMAELFYLSGILTVFFCGIVMSHYTWHNVTESSRVTTRHSFA 306
                                                                                                                                                                                                                                                                                                            MFETLQQFQGKT-----LHFFTLFSGIGIFIITFFISLLIGVSIGLITALLLKYSYLRR
                                                                            SNLLNKFHRQRNGNLIDHIPYSYQMMLFWAGL-RGAVGVALA-----AGFEG--ENAQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    569 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20.1%; Score 556; DB 20; Length 569; ilarity 28.9%; Pred. No. 5.1e-47; Conservative 119; Mismatches 181; Indels 98;
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99US-0116111.
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Search completed: October 18, 2002, 12:25:19 Job time : 38 secs

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Result
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A;Reference number: Z14440
A;Accession: T01804
A;Status: translated from GB/EMBL/DDBJ
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540	680	650	650	581	565	490	517	458	682	682	527	550	575	528	531
۳	N	N	N	N	N	N	N	2	N	2	N	N	N	N	2
S76231	F89832	AI1368	AB1738	G83189	H82610	F84154	AC2070	H75278	AC1532	AC1175	AE2932	в98350	D96585	T34941	D96827
Na+/H+-exchanging	hypoth				sodium/proton exch	Na+/H+ antiporter	Na+/H+ antiporter	probable Na+/H+ an	probable Na+/H+ an	probable Na+/H+ an	Na+/H+ antiporter	hypothetical prote	hypothetical prote	probable Na+/H+ an	protein F20B17.4 [

ALIGNMENTS

Arabidopsis thaliana #text_change 22-Oct-1999

A;Cross-references: EMBL:AF007271; NID:g2191181; PID:g2191184; GSPDB:GN00063; ATSP:A_A;Experimental source: cultivar Columbia C;Genetics: A;Map position: 5 A;Introns: 55/3; 95/2; 128/1; 148/1; 163/3; 240/3; 256/2; 286/3; 320/2; 400/3; 421/3 A; Gene: ATSP: A_TM021804.4 A; Map position: 5 A; Molecule type: DNA A; Residues: 1-457 < DAN> Query Match VMSHYTWHNVTESSRVTTRHSFATLSFVAETFIFLYVGMDALDIEKWKFVKNSQGLSVAV CSIISFGAVKIFKHLDIDFLDFGDYLAIGAIFAATDSVCTLQVLSQDETPLLYSLVFGEG GLLCAYIIKKLYFG-----RHSTDREVALMMLMSYLSYIMAELFYLSGILTVFFCGI VVNDATSVVVFNATQSFDLTHLNHEAAFHLLGNFLYLFLLSTLLGAAVSPLFSSLPFFLT GLISAYVIKKLYFGRWPHINCHRHSTDREVALMMLMAYLSYMLAELFDLSGILTVFFCGI LDSLVSKLPSLSTSDHASVVALNLFVALLCACIVLGHLLEENRWMNESITALLIGLGTGV **VMSHYTWHNVTESSRITTKHTFATLSFLAETFIFLYVGMDALDIDKWRSVSDTPGTSIAV** Similarity Conservative 62.6%; 44; Score 1732.5; DB 2; Pred. No. 2.4e-123; 4; Mismatches 46; Indels Length 457; 21; Gaps 241 181 361 301 283 231 183 61 63 ω ··

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A;Reference number: Z20226
A;Accession: T26529
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-703 <WIL>
A;Residues: eMBL: AL034393; PIDN:CAA22320.1; CE:
A;Experimental source: clone Y18D10A
C;Genetics:
A;Genet CESP:Y18D10A.6
A;Introns: 23/3; 56/1; 103/2; 246/3; 352/3; 492/2; 578,
RESULT 3
$66734

R; Dietrich, F.S.

R; Dietrich, F.S.

R; Dietrich to the EMBL Data Library, August 1995

A; Reference number: $69535

A; Accession; $69734
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-569 <MUR>
A;Residues: 1-569 <MUR>
A;Cross-references: EMBL:Z97208; PIDN:CAB10103.1; GSPDB:GN00066; SPDB:SPAC15A10.06
A;Cross-references: strain 972h-; cosmid c15A10
                                                                            R;Murphy, L.; Harris, D.; Wood, V.
submitted to the EMBL Data Library
A;Reference number: Z21738
A;Accession: T37706
A;Status: preliminary; translated
                                                                                                                                              probable sodium/hydrogen exchanger - fission yeast C;Species: Schizosaccharomyces pombe C;Date: 03-Dec11999 #sequence_revision 03-Dec-1999 C;Accession: T37706 R;Murphy, L.; Harris, D.; Wood, V.; Barrell, B.G.;
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A;Map position: 4R
C;Superfamily: hypothetical protein yvgP
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A; Residues: 1-633 <D
A; Cross-references:
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NESITALIIGLCTGVVILLLSGGKSSHLLVFSEDLFFIYLLPPIIFNAGFQVKKKQFFVN 108
                                                                                                                                                                                                                                                                                                                                      FDDSFMRPVF
                                                                                                                                                                                                                                                                                                                                                                      AVSSNKNLPNNISTIGGNIFGGLNETENTSPNPARSSMDKRNLRDKLGTIFNSDSQWFQN 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I---SICVARWCAVFPLSQFVNWIYRVKTIRSMSGITGENISVPDEIPYNYQMMTFWAGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ILVGLILVGRAAFVFPLS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KHYAYYNMSRRSQITIKYIFQLLARLSENFIFIYLGLELFTEVELVY----KPLLIIVAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -RGAVGVALALGIQGEYKFT---
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                                                                                                                                                                                                                                                                                                       609
                                                                                                                                                                                                                                                                                                                                      523
                                                                                                                                    : Wood, V.;
ca Library,
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                                                                                                                                     June
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                                                                                   GB/EMBL/DDBC
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No. 3.
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                                                                                                                                                                                                                       (Schizosaccharomyces
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A;Cross-references: EMBL:Z69646; PIDN:CAA93476.1; GSPDB:GN00028; CESP:F57C7.2
A;Experimental source: clone F57C7
C;Genetics:
                                                                  A;Gene: CESP:F57C7.2
A;Map position: X
A;Introns: 33/3; 81/3
                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-629 <WIL>
                                                                                                                                                                                                                submitted to the EMBL Data A; Reference number: 219625 A; Accession: T22848
                                                                                                                                                                                                                                                                                hypothetical protein F57C7.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #t.C;Accession: T22848
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A:Map position: 1
A:Introns: 11/1; 116/3; 356/3
C;Superfamily: hypothetical protein yvgP
                                                                                                                                                                                            A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                    R; White,
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Best Local
     Matches
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     Local Similarity les 158; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91
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                                                                                                                                                                                                                                                                                                                                                                                                                SRDDQAQWLTRFDEEVIKPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MITSTVTVVLFSTVVFGLMTKPLINLL----------LPPHKQMPS---GHSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMNLFVALLCACIVLGHLL-----EENRWVNESITALIIGLCTGVVILLLSGGKSSHL 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SFLSNLAKK----NSSDKISFRQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENA-I 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SFLNFENLSMTFVEALSMGATLSATDPVTVLAIFNSYKVDQKLYTIIFGESILNDAVAIV 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KHLDIDFLD--FGDYLAIGAIFAATDSVCTLQVL-SQDETPLLYSLVFGEGVVNDATSVV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVFSEDLFFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTLISCSIISFGA-VKIF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                             PTHTVHRYWRKFDDSFMRPV 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MELSDASAEPVVVDQQFTTEHFDEGNIAPTLSKKVSS----TFEQYQRAAGAFNQFFHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MTTSEPS-----SPKHF----TVPLLDNQPDSESDMITGPEVARPT-ALRMLLRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SNLLNKFHRQRNGNLIDHIPYSYQMMLFWAGL-RGAVGVALA----AGFEG--ENAQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLAQLSENFIFIXLGMSLFTQVDLVYKPIFILIT---TVAVTA-----SRYMNVFPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLSFVAETFIFLYVGMDALD----IEKWKFVKNSQGLSVAVSSILVGLILVGRAAFVFPL 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YPS-IESCIILLMAYTSYFFSNGCHMSGVVSLLFCGITLKHYAFFNMSYKAKLSTKYVFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LFNAIQSFDMTSFDPKIGLHF-----IGNELYLFLSSTFLGVGIGLLCAYIIKKLYFGR 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSFHSTYFFNVLLPPIILNSGYELHQSNFFRNIGTILTFAFAGTFISA--VTLGVLVYIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRATTLYVVVLTLIIFGGTTARMLEILHIETGVAADVDSDTEIGMLPWQQSPEFDLENSA
                                                             81/1; 119/2; 155/3; 207/2; 239/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                          #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                 20.0%;
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                                                                                                                                                                                                                                               Library,
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     77;
 Score 552.5; DB 2;
pred. No. 5.3e-34;
77; Mismatches 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 556; DB 2;
Pred. No. 2.5e-34;
9; Mismatches 181
                                                                                                                                                                                                                                             February
                                                               274/2;
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                              Length 629;
 Indels
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                                                             304/1;
53;
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                                                             354/1; 386/3; 421/3;
Gaps
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16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Na+/H-exchanging protein NHE-2 - rat C; Species: Rattus norvegicus (Norway rat) C;Date: 03-May-1994 #sequence_revision 03-Ma C;Accession: A46748; A47449 C;Accession: A010-848; A47449 R;Wang, Z.; Orlowski, J.; Shull, G.E. J. Biol. Chem. 268, 11925-11928, 1993 A;Title: Primary structure and functional ex A;Reference number: A46748; MUID:93280160
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A; Note:
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                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-813 <WAN>
                                                                                                                                                                                                                                                           A; Molecule type: nucleic acid
A; Residues: 117-813 <COL>
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                                                                                                                                                                                                                                          A; Experimental source: intestine
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                                                                                                                                                        Query Match
Best Local Similarity
               128
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                                                                                                                                                                                                                           sequence
           GVDEKSPPAMKTDVFFLYLLPPIVLDAGYFMPTRPFFENLGTIFWYAVVGTLWNSIGIGL
                                  GGKSSHLLVFSEDLFFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTL----ISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IRRR---PKIPKRYQHMILFAGL-RGAMAFALA-----
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                                                                                                                                            Conservative
                                                                                                                                                          17.5%;
28.0%;
                                                                                                                                            66;
                                                                                                                                          Score 485.5; 1
Pred. No. 8.3e
86; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression
                                                                                                                                          .3e-29;
les 215;
                                                                                                                                                                           DB 2;
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A;Cross-references: GB:L11236; NID:9205318; PIDN:AAA72350.1; PID:9205319 R;Collins, J.F.; Honda, T.; Knobel, S.; Bulus, N.M.; Conary, J.; DuBois, Proc. Natl. Acad. Sci. U.S.A. 90, 3938-3942, 1993 A;Title: Molecular cloning, sequencing, tissue distribution, and function A;Reference number: A47449; MUID:93248205 A;Accession: A47449
                                                 14 LFTSDHASV---VSMNLFVALLCACIVLGHLLEE-NRWVNESITALIIGLCTGVVILLLS
                                                                                                                                                                                                       sequence inconsistent with the nucleotide translation sequence extracted from NCBI backbone (NCBIN:130778, NCBIP:130779)
VFTLDYPHVQIPFEITLWILLASLAKIGFHLYHKLPTIVPESCLLIMVGLLLGGIIF--- 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FSTV-VFGLMTKPLINLLLPPH-KQMPSGHSSMTTSEPSSPKHFTVPLLDNQPDSESDMI 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAKKNSSDKISFRQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMITSTVTVVL 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIMESFIFCYIGVSV-----FVTNNQRWS--FSFLLFSLISITASRALFVYPLSWLLN
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Na+/H+-exchanging protein NHE-2 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 28-Feb-1997
C;Accession: A46747
R;Tse, C.M.; Levine, S.A.; Yun, C.H.; Montrose, M.H.; Little, P.J.; Pouysse, Title: Cloning and expression of a rabbit cDNA encoding a serum-activated A;Reference number: A46747; MUID:93280159
A;Accession: A46747
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-809 <TSS:
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                 -CFTLAFCLIWRA
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C;Accession: A40205
R;Tse, C.M.; Brant, S.R.; Walker, M.S.; Pouyssegur, J. Biol. Chem. 267, 9340-9346, 1992
A;Title: Cloning and sequencing of a rabbit cDNA enc A;Reference number: A40205; MUID:92250540
A;Accession: A40205
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Na+/H+-exchanging protein 3 - rabbit
Na+/H+-exchanging protein 3 - rabbit
Na+/H+ antiporter
C:Spacies: Oryctolagus cuniculus (domestic rabbit)
C:Date: 28-Aug-1992 #sequence_revision 28-Aug-1992
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A; Residues: 1-832 <TSE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 VVSMNLFVALLCACIV-LGHLLEENRWVNESITALIIGLCTGVVILLLSGGKSSHLLVF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                         LFITAAIVVIFFTVFILGITIRPLVEFL----DVKRSNKKQQAVSEEIHCRFF-
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                            MITGPEVARPTALRMLLRTPTHTVHRY----WRKFDDSFM
                                                      IVVFFTVIFQGLTIKPLVQWL----KVKRSEHREPKLNEKLHGRAFDHIL-----SAIE
                                                                                                                                   VIEPGFVFIISYLSYLTSEMLSLSSILAITFCGICCQKYVKANISEQSATTVRYTMKMLA
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                                                                                                                                                                               SGAETIIFMFLGISAVDPLIWTW:
                                                                                                                                                                                                            FVAETFIFLYVGMDALDIEKWKFVKNSQGLSVAVSSILVGLILVG--RAAFVFPLSFLSN
                                                                                                                                                                                                                                                                                                    LYNVFQSFVTLGGDKVTGVDCVKGIVSFFVVSLGGTLVGVVFAFLLSLVTR---FTKHVR
                                                                                                                                                                                                                                                                                                                                LFNAIQSFDMTSFDPKIGLHF----IGNFLYLFLSSTFLGVGIGLLCAYIIKKLYFGRHST 249
                                                                                                                                                                                                                                                                                                                                                              IMGELKIGLLDF----LLFGSLIAAVDPVAVLAVFEEVHVNEVLFIIVFGESLLNDAVTVV
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                                                                                      TVVLFSTVVFGLMTKPLINLLLPPHKQMPSGHSSMTTSEPSSPKHFTVPLLDNQPDSESD
                                                                                                                                                                                                                                                                                                                                                                                         --KHLDIDFLDFGDYLAIGAIFAATDSVCTLQVLSQ-DETPLLYSLVFGEGVVNDATSVV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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 ----QIGHNYLRDKWANFDRRFL
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                                                                                                                                                                                 ----NTAFVLLTLLFVSVFRAIGVVLQTWLLN
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CAMP-activated Na+/H+-exchanging protein betaNHE - rainbow trout C. Species: Oncorhynchus mykies (rainbow trout) C. Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 28-Feb-1997 C. Accession: A46188 R. Borgese, F.; Sardet, C.; Cappadoro, M.; Pouyssegur, J.; Motais, R. Proc. Natl. Acad. Sci. U.S.A. 89, 6765-6769, 1992 A.; Title: Cloning and expression of a CAMP-activated Na+/H+ exchanger: evidence A. Reference number: A46188; MUID:92357712 A.; Accession: A46188
A. Status: preliminary; not compared with conceptual translation A.; Molecule type: nucleic acid
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B407204
Na+/H+-exchanging protein 3 - rat
Na+/H+-exchanging protein 3 - rat
N; Alternate names: Na+/H+ antiporter
C; Species: Rattus norvegicus (Norway rat)
C; Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 05-Nov-1999
C; Accession: B40204
R; Orlowski, J; Kandasamy, R.A.; Shull, G.E.
J. Biol. Chem. 267, 9331-9339, 1992
A; Title: Molecular cloning of putative members of the Na/H exchanger gene face.
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A;Cross-references: GB:M85300; NID:g205706; PIDN:AAA41702.1; C;Keywords: transmembrane protein
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A; Accession: B40204
A; Status: preliminary
A; Molecule type: mRNA
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Matches 146
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                                                                                                                                                                                                                                                                                                                    DSESDMITGPEVARPTALRMLLRTPTHTVHRY----WRKFDDSFMRPV 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYNVFESFVTLGGDAVTGVDCVKGIVSFFVVSLGGTLVGVIFAFLLSLVTR---FTKHVR
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Pred. No. 1.6e
89; Mismatches
                                                                                                                                                                                                                                                                                 -QIGHNYLRDKWSNFDRKFLSKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200;
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Na+/H+-exchanging protein - Chinese hamster
N;Alternate names: Na+/H+ antiporter; Na+/H+ exchanger
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
C;Accession: S30198; S29541
C;Accession: L; Pouyssegur, J.
Biochim. Biophys. Acta 1172, 343-345, 1993
A;Title: Nucleotide sequence of the Chinese hamster Na(+)/H(+) e
A;Reference number: S30198; MUID:93192332
                                                                                                            C; Keywords: glycoprotein; i
F;76,374,414/Binding site:
                                                                                                                                                                       A;Cross-references: EMBL:X68970; NID:g49472;
C;Genetics:
                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-822 <CO
                                                                                                                                                    A; Gene: NHE1
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A;Experimental source: cephalic kidney hematopoietic tissues
A;Note: sequence extracted from NCBI backbone (NCBIP:113525)
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25 MNLFVALLCACIVLGHLLEE-NRWVNESITALIIGLCTGVVILLLSGGKSSHLLVFSEDL 83
                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TVVFGLMTKPLINLLLPPHKQMPSGHSSMTTSEPSSPKHFTVPLLDNQPDSESDMITGPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKNSSDKISFRQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMITSTVTVVLFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VFVQGMTIRPLVELLAVKKKK------ESKPSINEEIHTEFLDH----
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                                                         Similarity
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                                                                                                                                                                                                         COU>
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                                                       16.9%; Score 467.5; DB 28.2%; Pred. No. 1.9e-27
                                                                                                          ion transport; membrane protein
carbohydrate (Asn) (covalent)
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Pred. No. 1.6e-27;
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                                                                          DB 2;
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ISLWILLACLMKIGFHVIPTISSIVPESCLLIVVGLLVGG--LIKGVGETPPFL--QSDV

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Na-/H-exchanging protein 2 - human
C:Species: Homo sapiens (man)
C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 28-May-1999
C;Accession: A57644
R;Ghishan, F.K.; Knobel, S.M.; Summar, M.
Genomics 30, 25-30, 1995
A;Title: Molecular cloning, sequencing, chromosomal localization, and tissue dis A;Reference number: A57644; MUID:96129297
A;Reference number: A57644
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-698 GHI>
A;Cross-references: GB:S81591; NID:g1478393; PIDN:AAB36180.1; PID:g1478394
C;Genetics:
A;Gene: GDB:SLC9A2
A;Cross-references: GDB:132596; OMIM:600530
A;Map position: 2q11.2-2q11.2
C;Keywords: transmembrane protein
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A57644
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 172 LIGILLGFIAAFTTR---FTHNIRVIEPLFVFLYSYLSYITAEMFHLSGIMAITACAMTM 228
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                               226 FLGVGIGLLCAYIIKKLYFGRHSTDREVALMMLMSYLSYIMAELFYLSGILTVFFCGIVM 285
                                                                             115 HVNEQLYILVFGESLLNDAVTVVLYNLFKSFCQMKTIQTVDVFAG---IANFFVVGIGGV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225 NIGLLDTLLFGSIISAVDPVAVVAVFEEIHINELLHILVFGESLLNDAVTVVLYHLFEEF 284
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                                                                                                                                                                                                                                           IIGLCTGVVILLLSGGKSSHLLVFSEDLFFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDKISFRQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMITSTVTVVLFSTVVF 433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --ANYD-SIGISDIFLGFLSFFVVALGGVFVGVVYGVIAAFTSR---FTSHIRVIEPLFV 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTLISCSIIS--FGAVKIFKHLDID
                                                                                               DETPLLYSLYFGEGVVNDATSVYLFNAIQSF----DMTSFDPKIGLHFIGNFLYLFLSST 225
                                                                                                                                                    AVVGTLWNSIGIGLSLFGICQIEAFGLSDITLL---QNLLFGSLISAVDPVAVLAVFENI 114
                                                                                                                                                                                  GAIGTL----ISCSIISFGAVKIFKHLDIDFLDFGDYLAIGAIFAATDSVCTLQVLSQ- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----DICGHYGHHHWKDKLNRFNKKYVK 563
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28.4%; Pred
tre 77;
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                                                                                                                                                                                                                                                                                       Score 466; DB 2; 1
Pred. No. 2.1e-27;
7; Mismatches 194;
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0.	Ov 201 DWTSFDDKTGHFTGNFLYLFLSSTFLGVGIGLLCAYIIKKLYFGRHSTDREVAL 255
Ü	Db 221 NIGLLDNLLFGSIISAVDPVAVLAVFEEIHINELLHILVFGESLLNDAVTVVLYHLFEEF 280
J	Qy 142 FLDFGDYLAIGAIFAATDSVCTLQVLSQDE-TPLLYSLVFGEGVVNDATSVVLFNAIQSF 200
J	Db 161 FFLFLLPPIILDAGYFLPLRQFTENLGTILIFAVVGTLWNAFFLGGLMYAVCLVGGEQIN 220
	Qy 84 FFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTLISCSIISFGAVKIFKHLDID 141
J	OY 25 MNLFVALLCACIVLGHLLEE-NRWVNESITALIIGLCTGVVILLLSGGKSSHLLVFSEDL 83 :: :: : : ::: : : : Db 105 ISLWILLACLMKIGFHVIPTISSIVPESCLLIVVGLLVGGLIKAVGETPPFLQSEV 160
22;	Query Match 16.6%; Score 460.5; DB 2; Length 818; Best Local Similarity 28.0%; Pred. No. 6.5e-27; Matches 145; Conservative 108; Mismatches 181; Indels 83; Gaps
	A;Residues: 1-682,'H',684-818 <re2> A;Cross-references: GB:M89631; NID:g164595; PIDN:AAA31092.1; PID:g164596</re2>
	A; Accession: 146613 A; Accession: 146613 A; Status: preliminary; translated from GB/EMBL/DDBJ
PK1 renal e	A. T. Physiol. 261, 1088-1094, 1991 A. J. Physiol. 261, 1088-1094, 1991 A. Title: cDNA cloning and immunolocalization of a Na+-H+ exchanger in LLC-PK1 A. Paferonce number: T46613
	Experime Note: se
•	A; MOLECULE LYPE: HIKNA A; Residues: 1-818 (REI)- A; Cross-references: GB:S71135; NID:g240706; PIDN:AAB20633.1; PID:g240707
	A;Accession: A48858 A;Status: preliminary
C-PK1 renal	Am. J. Physici. 261, F1008-F1094, 1931 A; Title: cDNA cloning and immunolocalization of a Na(+)-H+ exchanger in LLC A; Reference number: A48858; MUID:92087905
J.; Aronso	C;Accession: A48858; I46613 R;Reilly, R.F.; Hildebrandt, F.; Biemesderfer, D.; Sardet, C.; Pouyssegur,
ō	Na+/H+-exchanging protein - pig C;Species: Sus scrofa domestica (domestic pig) C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 01-Dec-2000
	RESULT 13 A48858
	Db 424 LR 425
	Qy 519 MR 520
	Db 386 EIHWCRFFDHVKTGIEDVCGHWGHNEWRDKFKKFDDKY 423
	Qy 463 PSSPKHETVPLLDNQPDSESDMITGPEVARPTALRMLLRTPTHTVHRYWRKFDDSF 518
	Db 333LLPATVFPRKKLEITAAIVVIFFTVFILGITIRPLVEFLDVKRSNKKQQAVSE 385
	Qy 403 KFTTSGHTSLHENAIMITSTVTVVLFSTVVFGLMTKPLINLLLPPHKQMPSGHSSMTTSE 462
	Db 280CFTLAFCLIWRALGVEVLTQVINWERTIPLTEKDQFIIAYGGL-RGAICFALVF- 332
	Qy 343 VSSILVGLILVGRAAFVFFLSFLSNLAKKNSSDKISFRQQIIIWWAGLMRGAVSIALAYN 402
	Db 229 NKYYEENVSQKSYTTIKYFMKMLSSVSETLIFIFMGVSTVGKNHEWNWAFV 279
	Qy 286 SHYTWHNVTESSRVTTRHSFATLSFVAETFIFLYVGMDALDIEKWKFVKNSQGLSVA 342

256 MMLMSYLSYIMAELFYLSGILTVFFCGIVMSHYTWHNVTESSRVTTRHSFATLSFVAETF 315 : | ||::|: ||:||: ||:|| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| | |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |:

281 --ANYD-RVGIVDIVLGFL-SFFVVSLGGVFVGVVYGVIAAFTSR---FTSHIRVIEPLF 333

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rabbit ileal villus

Potter

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RESULT 14
A40204
A40204
Na+/H+-exchanging protein 1 - rat
N; Alternate names: Na+/H+ antiporter
C; Species: Rattus norvegicus (Norway rat)
C; Date: 28-Aug-1992 #sequence_revision 28-Aug-1992
C; Accession: A40204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Orlowski, J.; Kandasamy, R.A.; Shull, G.E. J. Blol. Chem. 267, 9331-939, 1992
A;Title: Wolecular cloning of putative members rally related proteins.
A;Reference number: A40204
A;Recession: A40204
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Keywords: transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-820 <ORL>
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Best Local
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                                                                                                                                                                                                                                                    GLSVAVSSILVGLILVGRAAFVFPLSFLSNLAKKNSSDKISFRQQIIIWWAGLMRGAVSI
                                                                                                                                                                                                                                                                                                                                                                                                                              FLSSTFLGVGIGLLCAYIIKKLYFGRHSTDREVALMMLMSYLSYIMAELFYLSGILTVFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLSQDE-TPLLYSLVFGEGVVNDATSVVLFNAIQSFDMTSFDPKIGLH--FIG--NFLYL
                                                                                                                                                                                                                                                                                                                                          CGIVMSHYTWHNVTESSRVTTRHSFATLSFVAETFIFLYVGMDALDIE----KWKFVKNSQ
                                                                                                                                                                                                                                                                                                                                                                                    SLGGVFVGVVYGVIAAFTSR----FTSHIRVIEPLFVFLYSYMAYLSAELFHLSGIMALIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLGTILIFAVVGTLWNAFFLGGLLYAVCLVGGEQINNIGLLDTLLFGSIISAVDPVAVLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEWTIMLEGAIGTLISCSIIS--FGAVKIFKHLDIDELDEGDYLAIGAIFAATDSVCTLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VPESCLLIVVGLLVGG--LIKGVGETPPFL--QSDVFFLFLLPPIILDAGYFLPLRQFTE 188
                                                                                     MTTSEPSSPKHFTVPLLDNQPDSESDMITGPEVARPTALRMLLRTPTHTVHRYWR----K
                                                                                                                                  SLGY--LLDKKHFPMCD--LFLTAIITVIFFTVFVQGMTIRPLVDLLAVKKKQ---
                                                                                                                                                                       ALAYNKFTTSGHTSLHENAIMITSTVTVVLFSTVVFGLMTKPLINLLLPPHKQMPSGHSS
                                                                                                                                                                                                                 ----ISTLL--FCLIARVLGVLVLTWFIN---KFRIVKLTPKDQFIIAYGGL-RGAIAF
                                                                                                                                                                                                                                                                                                  SGVVMRPYVEANISHKSHTTIKYFLKMWSSVSETLIFIFLGVSTVAGSHQWNWTFV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VFEEIHINELLHILVFGESLLNDAVTVVLYHLFEEFASYEY---VGISDIFLGFLSFFVV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEVARPTALRMLLRTPTHTVHRYWR----KFDDSFMR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IFIFLGVSTVAGSHHWNWTFV------ISTLL--FCLIARVLGVLGLTWFIN---KF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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Pred. No. 7.1e-27;
98; Mismatches 180
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                                                  ----DICGHYGHHHWKDKLNR
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A; Residues: 472-816 < FLI>
A; Cross-references: EMBL: X56536; NID: g1666; PIDN: CAA39881.1; PID: g1667
A; Cross-references: EMBL: X56536; NID: g1666; PIDN: CAA39881.1; PID: g1667
A; Hildebrandt, F.; Pizzonia, J.H.; Reilly, R.F.; Reboucas, N.A.; Sardet, C.; Pouysseg Blochim. Biophys. Acta 1129, 105-108, 1991
A; Title: Cloning, sequence, and tissue distribution of a rabbit renal Na(+)/H(+) exch A; Reference number: S30602; MUID: 92096447
A; Accession: S30602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Na+/H+-exchanging protein - rabbit
N;Alternate names: Na+/H+ antiporter; Na+/H+ exchanger; pH regulatory protein
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 01-Dec-2000
C;Accession: S16328; S19926; S30602
R;Trse, C.M.; Ma, A.I.; Yang, V.W.; Watson, A.J.M.; Levine, S.; Montrose, M.H..
EMBO J. 10, 1957-1967, 1991
A;Title: Molecular cloning and expression of a cDNA encoding the rabbit ileal
A;Accession: S16328; MUID:91293066
A;Accession: S16328
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FEBS Lett. 279, 25-29, 1991
A;Title: Identification of the protein and
A;Reference number: S13926; MUID:91138752
A;Accession: S13926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X59935; NID:g1642; PIDN:CAA42558.1; R;Fliegel, L.; Sardet, C.; Pouyssegur, J.; Barr, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-816 <TSE>
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                                                                                                                                                                                                                                                                                                                                            MNLFVALLCACIVLGHLLEE-NRWVNESITALIIGLCTGVVILLLLSGGKSSHLLVFSEDL 83
MLMSYLSYIMAELFYLSGILTVFFCGIVMSHYTWHNVTESSRVTTRHSFATLSFVAETFI
                                                             --ANYDHVGIVDIVLGFL-SFFVVALGGVFVGVVYGVIAAFTSR---FTAHIRVIEPLFV
                                                                                                                                                                         FLDFGDYLAIGAIFAATDSVCTLQVLSQDE-TPLLYSLVFGEGVVNDATSVVLFNAIQSF
                                                                                                                                                                                                                                FFLFLLPPIILDAGYFLPLRQFTENLGTILIFAVVGTLWNAFFLGGLMYAVCLVGGEQIN
                                                                                                                                                                                                                                                                                                                  ISLWILLACLMKIGFHVIPTISSIVPESCLLIVVGLLVGGLIKGV-GEKPPFL---QSEV
                                                                                                                                               NIGLLDNLLFGSIISAVDPVAVLAVFEEIHINELLHILVFGESLLNDAVTVVLYHLFEEF 280
                                                                                                                                                                                                                                                                          FFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTLISCSIIS--FGAVKIFKHLDID 141
                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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Q9uby0 homo sapien
Q61165 mus musculu
P26433 rattus norv
Q1345 oncorhynchu
P26431 rattus norv
Q1345 oncorhynchu
P26431 rattus norv
P48761 cricetulus
Q28362 didelphis m
P48762 sus scrofa
P48763 homo sapien
P48764 homo sapien
P48764 homo sapien
P26434 rattus norv
Q14940 homo sapien
P26434 rattus norv
Q14940 homo sapien
P26434 rattus norv
Q15494 caenorhabdi
Q50678 mycobacteri
P32703 escherichia
Q14123 schizosacchar
Q6036 methanococc
P26235 enterococcu
Q99173 zygosacchar
Q58916 methanococc
P15812 podospora a
P44727 haemophilus
P34855 apis mellif
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Q04121 saccharomyc
P48763 rattus norv
P50482 oryctolagus
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Mitochondrial sodium/hydrogen exchanger (Mito
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
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                                                                                                                                                                                                                              MWYNFDHNYLKPLLTHSG
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3402
4402
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4407
                                       Saccharomycetaceae;
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                                                                                                                                                                                                                                                                            -HIRVGV----
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Pred. No. 7.
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                                       Saccharomyces
                                                                                                    (Mitochondrial
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Best Local 9
Matches 160
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-I- FUNCTION: ELECTRONEUTRAL EXCHANGE OF PROTONS F-1- FUNCTION: ELECTRONEUTRAL INNER MEMBRANE. CONTRIBUTES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M., Hunicke-Smith S., Hyman R., Komp C., Lashkari D., Lew H. Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., P. Roberts D., Schramm S., Schroeder M., Shogren T., Shroff Winant A., Yelton M., Botstein D., Davis R.W.; Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGD;
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                                                                                                                                                           FMTIMLEGAIGTLISCSIISEGAVKIEKHLDIDELD--FGDYLAIGAIFAATDSVCTLQV
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SHYTWHNVTESSRVTTRHSFATLSFVAETFIFLYVGMDALDIEKWKFVKNSOGLSVAVSS
                                                      FLGVGIGLLCAYIIKKLYFGRHSTDREVALMMLMSYLSYIMAELFYLSGILTVFFCGIVM
                                       LIGVLIGILVALLLKHTHIRRY-PQIESCLILLIAYESYFFSNGCHMSGIVSLLFCGITL
                                                                                         FNAYKVDPKLYTIIFGESLLNDAISIVMFETCQKFHGQPATFSSVFEGAGLFLMTFSVSL
                                                                                                                   LSQDET-PLLYSLVFGEGVVNDATSVVLFNAIQSFDMTSFDPKIGLHFIGNFLYLFLSST
                                                                                                                                               MLSILIFAIPGTFISAVVIGI-ILYIWTFLGLESIDISFADAMSVGATLSATDPVTILSI
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4; NAHEXCHNGR.
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27.2%;
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Pred. No. 3.3e-29;
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9B771ABDE41CEB0A CRC64;
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exchanger.
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h C., Petel 1
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PAB763; Q16434;
PAB763; Q16434;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-4001 (Rel. 40, Last annotation update)
                                                                                                              Ghishan F.K., Knobel S.M., Summar M.;

"Molecular cloning, sequencing, chromosomal localization, and distribution of the human Na+/H+ exchanger (SLC9A2).";

Genomics 30:25-30(1995).

-I- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GE BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE I SODIUM ION CHEMICAL GRADIENT. SEEMS TO PLAY AN IMPORTANT COLONIC SODIUM ABSORPTION.
                                                                                                                                                                                                                                                                                                                                   Dubois R., Ghishan F.K.;
"Molecular cloning, sequencing, tissue distribution, expression of a Nat/H+ exchanger (NHE-2).";
Proc. Natl. Acad. Sci. U.S.A. 90:3938-3942(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang 2., Orlowski J., Shull G.E.;
"Primary structure and functional expression gastrointestinal isoform of the rat Na/H exci J. Blol. Chem. 268:11925-11928(1993).
                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-93248205; PubMed-7683411; Collins J.F., Honda T., Knobel S.
                                                                                                                                                                                                                                                                                                                                                                                                                              [2]
SEQUENCE FROM N.A. (SHORT ISOFORM).
STONTH-SPRAGUE-DAWLEY; TISSUE-Small intestine;
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                                                                                                                                                                                                                                                                     MEDLINE=96129297; PubMed=8595899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (SHORT ISOFORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-93280160; PubMed-7685026; Wang Z., Orlowski J., Shull G.E.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116
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        SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: PREDOMINANTLY IN SMALL INTESTINE, COLON, STOMACH, WITH MUCH LOWER LEVELS IN SKELETAL MUSCLE, KIDNEY, ETESTIS, UTERUS, HEART, AND LUNG.
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(POSSIBLE).
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                                                                                                                                                                                                                                                                                                                                                                                                     S., Bulus N.M., Conary J.,
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Best Local Similarity
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EMBL; S81591;
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between
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   188
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                                                                                                14 LFTSDHASV----VSMNLFVALLCACIVLGHLLEE-NRWVNESITALIIGLCTGVVILLLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY. CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS. CAUTION: REF.3 SEQUENCE WAS ORIGINALLY THOUGHT TO ORIGINATE FROM
SLFGICQIEAFGLSDITLL---QNLLFGSLISAVDPVAVLAVFENIHVNEQLYILVFGES
                   SIISFGAVKIFKHLDIDFLDFGDYLAIGAIFAATDSVCTLQVLSQ-DETPLLYSLVFGEG
                                        GVDEKSPPAMKTDVFFLYLLPPIVLDAGYFMPTRPFFENLGTIFWYAVVGTLWNSIGIGL
                                                          GGKSSHLLVFSEDLFFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTL----ISC
                                                                              VFTLDYPHVQIPFEITLWILLASLAKIGFHLYHKLPTIVPESCLLIMVGLLLGGIIF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00999; Na_H_Exchanger;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L11236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PR01084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the Swiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rane; Glycoprotein; Sodium transport; Transport;
family; Phosphorylation; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR000676; NaH_Exchngr.
                                                                                                                                                           786
813 AA;
                                                                                                                     Conservative
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161
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AAB36180.1;
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                                                                                                                                                        Institute of Bioinformatics
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80
101
107
128
139
160
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28.0%;
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                                                                                                                     6;
                                                                                                                    Score 485.5;
Pred. No. 7.6e
86; Mismatches
                                                                                                                                                                   A -> P (IN REF. 3).
V -> G (IN REF. 2).
                                                                                                                                                                                                  MISSING
                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
G (M5B) (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                D (M4) (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

E (M5) (POTENTYAT'
                                                                                                                                                                                                                                                                              CYTOPLASMIC K (M9) (POTE
                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).

B (M2) HYDROPHOBIC.

CYTOPLASMIC (POTENTIAL).

C (M3) (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
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F (M5A) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                            C (M3) (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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A (M1) HYDROPHOBIC
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EXTRACELLULAR (POT
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VTOPLASMIC (POTENTIAL).
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HW (IN REF. 3)
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NAH2_RABIT
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p50482;
p50482;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Sodium/hydrogen exchanger 2 (Na(+)/H(+) exchanger
SLC9A2 OR NHE2.
                                                                                                                               the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                             J. B101. Chem. 268:11917-11924(1993).
-i- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD SODIUM ION CHEMICAL GRADIENT. SEEMS TO PLAY AN IMPORTANT ROLE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning and expression of a rabbit cDNA encoding a serum-activated ethylisopropylamiloride-resistant epithelial Na+/H+ exchanger isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93280159; PubMed=7685025;
Tse C.-M., Levine S.A., Yun C.H., Montrose M.H., Little Pouyssegur J., Donowitz M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
STRAIN=NEW ZEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eu
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus
 Transmembrane;
                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAH2_RABIT
                 PRINTS;
                                                             EMBL; L13733; -; NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9986;
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                                              InterPro;
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                                                                                                                                                                                                                                                PTM: PHOSPHORYLATED (POSSIBLE).
SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF H
                                                                                                                                                                                                                                                                                               COLONIC SODIUM ABSORPTION.
SUBCELLULAR LOCATION: Integral membrane
TISSUE SPECIFICITY: HIGH LEVELS IN INTES
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                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTRHSFATLSFVAETF1FLYVGMDALDIE---KWKFVKNSQGLSVAVSSILVGLILVGRA
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                              Pro; IPR000676; NaH_Exchngr.
PF00999; Na_H_Exchanger; 1.
                  PR01084;
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Glycoprotein;
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Sodium transport; Transport; Symport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                               membrane protein.
IN INTESTINE AND KIDNEY
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                                                                                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                There are no restrictions ong as its content is in
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                                                      IMITSTVTVVLFSTVVFGLMTKPLINLLLPPHKQMPSGHSSMTTSEPSSPKHFTVPLLDN
                                                                                                                                                                                                          VVNDATSVVLENAIQSE----DMTSEDPKIGLHFIGNFLYLFLSSTFLGVGIGLLCAYII
                  QPDSESDMITGPEVARPTALRMLLRTPTHTVHRYWR----KFDDSFMR
                                                                          LGVEVLIRVINWER---TIPLTEKDQFITAYGGL-RGAICFALVE----LLPAAVFPRKK 458
                                                                                                                                                    R---FTHNIRVIEPLFVFLYSYLSYITAEMFHLSGIMAITACAMTMNKYVEENVSQKSYT
                                                                                                                                                               KKLYFGRHSTDREVALMMLMSYLSYIMAELFYLSGILTVFFCGIVMSHYTWHNVTESSRV
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                                                                                                                                                                                                                                                                                   GGKSSHLLVFSEDLFFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTL-----ISC 124
                                                                                                                                                                                                                                                                                                       VFTLDYPHVQIPFEITLWILLASLAKIGFHLYHKLPTIVPESCLLIMVGLLLGGIIF---
VKTGIEDVC-
                                                                                           AFVFPLSFLSNLAKKNSSDKISFRQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENA
                                                                                                                TIKYFMKMLSSVSETLIFIFMGVSTVGKNHEWNWAFV-----
                                                                                                                                  TTRHSFATLSFVAETFIFLYVGMDALDIE---KWKFVKNSQGLSVAVSSILVGLILVGRA
                                                                                                                                                                                        LLNDAVTVVLYNLFKSFCQMKTIETIDVFAG
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                                     LFITAAIVVIFFTVFILGITIRPLVEFL
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147; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                 90744 MW;
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                                                                                                                                                                                                                                                                                                                                                   Score 482.5;
Pred. No. 1.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
C (M3) (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL)
J (M8) (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                              M (M11) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                    L (M10) (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                       K (M9) (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H (M6) (POTENTIAL)
CYTOPLASMIC (POTENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
G (M5B) (POTENTIAL).
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E (M5) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D (M4) (POTENTIAL)
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B (M2) (POTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A (M1) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        I (M7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                  DBD00B45443D87A6 CRC64;
-GHWGHNFWRDKFKKFDDKYLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                          ---IANFFVVGIGGVLIGIFLGFIAAFTT
                                     DVKRSNKKQQAVSEEIHCRFF
                                                                                                                                                                                                                                                                                                                                             1.2e-23;
nes 216;
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                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
                                                                                                                 -CFTLAFCLIWRA
                    520
                                                                                                                                                                                                                                                                                                                                                                809;
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                                       Ä
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                               416
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18;

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EMBL; AF073299; , EMBL; AC007239; , MIM; 600530; -.
                                                             TRANSMEM
DOMAIN
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Sodium/hydrogen exchanger 2 (Na(+)/H(+) exchanger
SLC9A2 OR NHE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HUMAN
      TRANSMEM
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                                                                                                                                                                                                                      Multigene
                                                                                                                                                                                                                                   Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ramaswamy K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-99375108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9UBY0;
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAH2_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Malakooti J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD SODIUM ION CHEMICAL GRADIENT. SEEMS TO PLAY AN IMPORTANT ROLE IN
                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY. CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COLONIC SODIUM ABSORPTION.

SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: EXPRESSED IN SKELETAL MUSCLE,
KIDNEY. LOWER LEVELS IN THE TESTIS, PROSTATE, OVA
                                                                                                                                                                                                                                                                           AD41635.1; AC007239; AAF19248.1; 600530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lecular cloning, tissue distribution,
human Na(+)/H(+) exchanger NHE2.";
J. Physiol. 277:G383-G390(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTESTINE.
                                                                                                                                                                                                                                           PR01084; NAHEXCHNGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wohldmann
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                                                                                                                                                                                                                                                      IPR000676; NaH_Exchngr.
                                                                                                                                                                                                                      family;
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1190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P.;
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dal R.Y., Schmidt
                                                                                                                                                                                                                     Phosphorylation
  13
33
79
100
106
1127
1138
1159
1168
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229
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F (M5A) (POTENTIAL)

F (M5A) (POTENTIAL)

CYTOPLASMIC (POTENTIAL).

G (M5B) (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

H (M6) (POTENTIAL).

CYTOPLASMIC (POTENTIAL)

I (M7) (POTENTIAL)
                                                                      CYTOPLASMIC (POTENTIAL).

A (M1) HUDROPHOBIC.

CYTOPLASMIC (POTENTIAL).

B (M2) HYDROPHOBIC.

CYTOPLASMIC (POTENTIAL).

C (M3) (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

E (M5) (POTENTIAL).

E (M5) (POTENTIAL).

E (M5) (POTENTIAL).
                                                                                                                                                                                                                              Sodium transport; Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata;
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      EXCHANGER FAMILY.
DENOMINATION OF HYDROPHOBIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        functional
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OVARY,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                      JOQILIII,
SLC9A1 OR NHEL.
Mus musculus (Mouse).
Mus musculus (Motazoa; Chordata;
heria; Rodentia;
Dewey M.J., Bowman L.H.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GI
BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
                                                                                                                                   NAH1_MOUSE STANDARD; PRT; 820 AA. 061165; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) sodium/hydrogen exchanger 1 (Na(+)/H(+) exchanger SLC9A1 OR NHE1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
TRANSMEM
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DOMAIN
                                                                                                                                                                                                                         MOUSE
                                                  STRAIN-BALB/C;
                                                               SEQUENCE FROM
                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGVVILLLSGGKSSHLLVFSEDLFFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIG 119
                                                                                                                                                                                                                                                                       ~EIYCRLFDHVKTGIEDVC------------GHWGHNFWRDKFKKFDDKYLR
                                                                                                                                                                                                                                                                                             KHFTVPLLDNQPDSESDMITGPEVARPTALRMLLRTPTHTVHRYWR----KFDDSFMR
                                                                                                                                                                                                                                                                                                                                                                                  EENVSQKSYTTIKYFMKMLSSVSETLIFIFMGVSTVGKNHEWNWAFV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                            WHNVTESSRVTTRHSFATLSFVAETFIFLYVGMDALDIE---KWKFVKNSQGLSVAVSSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLGFIAAFTTR---FTHNIRVIEPLFVFLYSYLSYITAEMFHLSGIMAITACAMTMNKYV
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27.98;
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EXTRACELLULAR (I
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Pred.
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N-LINKED (GLCNAC. . .)
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J (M8) (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

K (M9) (POTENTIAL).
                                                                                              Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17EE177DC3830D0A CRC64;
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. No. 1.4e-23;
ismatches 220;
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                                                                                                Euteleostomi;
; Murinae; Mus
                                                                                                                                               (NHE-1).
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               GENERATED
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Matches
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DOMAIN
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000676; NaH_Exchngr.
Pfam; PF00999; Na_H_Exchanger; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG CAUTION: HYDROPHOBIC DOMAINS A, B AND L ARE NOT TRANSMEMBRANAL, BUT ONLY MEMBRANE-ASSOCIATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTM: PHOSPHORYLATED (POSSIBLE).
SIMILARITY: BELONGS TO THE NA(+)/H(+)
CAUTION: THE NUMBER, LOCALIZATION AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Integral
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 DMTSFDPKIGLH--FIG--NFLYLFLSSTFLGVGIGLLCAYIIKKLYFGRHSTDREVALM
                       NIGLLDTLLFGSIISAVDPVAVLAVFEEIHINELLHILVFGESLLNDAVTVVLYHLFEEF
                                                                                                      ISLWILLACLMKIGFHVIPTISSIVPESCLLIVVGLLVGG--LIKGVGETPPFL--QSDV
                                                                                                                                    MNLFVALLCACIVLGHLLEE-NRWVNESITALIIGLCTGVVILLLSGGKSSHLLVFSEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGI:102462;
                                             FLDFGDYLAIGAIFAATDSVCTLQVLSQDE-TPLLYSLVFGEGVVNDATSVVLFNAIQSF
                                                                    FFLFLLPPIILDAGYFLPLRQFTENLGTILIFAVVGTLWNAFFLGGLLYAVCLVGGEQIN
                                                                                          FFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTLISCSIIS--FGAVKIFKHLDID 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PR01084;
                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                non-profit institutions as long as its content and this statement is not removed. Usage by an
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28.4%;
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                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (P 0589C4D08DD348BE CRC64;
                                                                                                                                                                        Pred.
                                                                                                                                                                                                                                                                                   CYTOPLASMIC K (M9) (POTE
                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL)

J (M8) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                          H (M6) (POTENTIAL)
CYTOPLASMIC (POTEN
                                                                                                                                                                                                                                                                                                                                                                            G (M5B) (PO
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E (M5) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
C (M3) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL)
B (M2) HYDROPHOBIC.
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                                                                                                                                                                                 Score 472.5;
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F (M5A) (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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DENOMINATION OF HYDROPHOBIC
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                                                                                                                                                            189;
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or send a
                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and the modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                     Tise C.-M., Brant S.R., Walker S.S., Pouyssegur J., Donowitz M.;
"Cloning and sequencing of a rabbit cDNA encoding an intestinal and
kidney-specific Na+/H+ exchanger isoform (NHE-3).";
J. Biol. Chem. 267:9340-9346(1992).

-i- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-NEW ZEALAND WHITE; TISSUE-Ileal villus, and Kidney cortex; MEDLINE-92250540; PubMed-1374392; TSe C.-M., Brant S.R., Walker S.S., Pouyssegur J., Donowitz M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-AUG-1992 (Rel.
01-AUG-1992 (Rel.
15-JUL-1999 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; 
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLC9A3 OR NHE3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sodium/hydrogen exchanger
                                                 EMBL; M87007; AAA31
PIR; A40205; A40205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9986;
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                                                                                                                                                                                                                                        DESCENDING COLON.

PTM: PHOSPHORYLATED (POSSIBLE).

SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.

SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.

CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HY

DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Integral membrane protein:
TISSUE SPECIFICITY: INTESTINA AND KIDNEY SPECIFIC. MOST ABUNDANT
IN KIDNEY CORTEX, FOLLOWED EQUALLY BY ILEUM AND ASCENDING COLON,
THEN KIDNEY MEDULLA AND JEJUNUM. IS ABSENT FROM DUODENUM AND
                                                                                                                                                                                                                                                                                                                                                                                                            TRANSDUCTION.
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                                                                                                    s requires a license agreement (S an email to license@isb-sib.ch).
                                                                     AAA31420.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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(Na(+)/H(+) exchanger
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AND DENOMINATION OF HYDROPHOBIC
                                                                                                                         (See http://www.isb-sib
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Pfam; PF00999; Na_ PRINTS; PR01084; N

InterPro; IPR000676; NaH_Exchngr.
Pfam; PF00999; Na_H_Exchanger; 1.
PRINTS; PR01084; NAHEXCHNGR.

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  RESULT
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Best Local S
Matches 148
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                                                                                                                                                                                                                                                                                                        22 VVSMNLFVALLCACIV-LGHLLEENRWVNESITALIIGLCTGVVILLLSGGKSSHLLVF-
                                                                                                                                                                  DREVALMMLMSYLSYIMAELFYLSGILTVFFCGIVMSHYTWHNVTESSRVTTRHSFATLS
                          DISG
                                                                                        RYRMVQLELI----DQVVMSYGGL-RGAVAFALVALLDGNK-----VKEKNLFVSTTI
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                                                                                                                                                                                                                                                                                         IIALWVLVASLAKIVFHLSH--KVTSVVPESALLIVLGLVLGGIVL----AADHIASFT
                                        MITGPEVARPTALRMLLRTPTHTVHRY - - - - WRKFDDSFM
                                                                       TVVLFSTVVFGLMTKPLINLLLPPHKQMPSGHSSMTTSEPSSPKHFTVPLLDNQPDSESD
                                                                                                        LAKKNSSDKISFRQQIIIWWAGLMRGAVSIALAY - - - - NKFTTSGHTSLHENAIMITSTV
                                                                                                                        SGAETIIFMFLGISAVDPLIWTW------NTAFVLLTLLFVSVFRAIGVVLQTWLLN
                                                                                                                                                        VIEPGFVFIISYLSYLTSEMLSLSSILAITFCGICCQKYVKANISEQSATTVRYTMKMLA
                                                                                                                                                                                        LYNVFQSFVTLGGDKVTGVDCVKGIVSFFVVSLGGTLVGVVFAFLLSLVTR----FTKHVR
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                                                                                                                                                                                                                                                        LTPTVFFFYLLPPIVLDAGYFMPNRLFFSNLGSILLYAVVGTVWNAATTGLSLYGVFLSG
                                                                                                                                                                                                                                                                         -SEDLFFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTLISCSIISFGAVKIF---
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EXTRACELLULAR (POTENTIAL).

M6 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

M7 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

M8 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
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#2 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

#3 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

#4 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR ()
M5A (POTENTIAL)
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Pred. No. 6.1
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N-LINKED (GLCNAC .) (
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M1 (POTENTIAL)
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                                                         ·KVKRSEHREPKLNEKLHGRAFDHIL-
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                                                                                                                                                                                                                                                                                                                          197;
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                                                                                                                                                                                                                                                                                                                                           832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Symport;
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                                                        SAIE
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Multigene fami
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                                                                                                                                                                                                                Pfam; PF00999;
                                                                                                                                                                                                                                                                                                  between
                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biol.
                                                                                                                                                                                                         PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-92250539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                      nterPro;
                                                                                                                                                                                                                                                                                         European
                                                                                                                                                                                                                                                                                                                                                                                  TRANSDUCTION.
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Orlowski J., Kandasamy R.A., Shull G.E.; "Molecular cloning of putative members of the Na/H family, cDNA cloning, deduced amino acid sequence, expression of the rat Na/H exchanger NHE-1 and two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sodium/hydrogen exchanger SLC9A3 OR NHE3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAH3_RAT STANDARD; PRT; 831 AA
P26433;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               related proteins.";
J. Biol. Chem. 267:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
                                                                                                                                                                    PTM: PHOSPHORYLATED (POSSIBLE).
SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HY
DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Integral mer
TISSUE SPECIFICITY: MOST ABUNDANT
                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS, MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
                                                                                                                                                                                                                                                                                FOLLOWED BY KIDNEY AND STOMACH
                                                                                              SWISS-PROT entry is copyright. It is produced through a centre the Swiss Institute of Bioinformatics and the EMBL
                       non-profit institutions as long and this statement is not removed.
                                                                    Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267:9331-9339(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=1577762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           t annotation update)
3 (Na(+)/H(+) exchanger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                     membrane protein.
ANT IN COLON AND SMALL
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                                               as its content
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                                                                                                                                                                                               FAMILY.
                                                                    restrictions
                       and
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                                                                                                   a collaboration -
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entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).

TRANSMEM DOMAIN TRANSMEM DOMAIN EMBL; M85300; AAA41702.1; -. PIR; B40204; B40204. 19: B40204. 1PR000676; NaH_Exchngr. 19: Na H Exchanger; 1. Glycoprotein; NAHEXCHNGR. Phosphorylation 96 109 130 130 157 177 177 199 229 229 229 227 229 271 287 337 359 366 25 51 76 CYTOPLASMIC (POTENTIAL).

B (M2) HYDROPHOBIC.
CYTOPLASMIC (POTENTIAL).
C (M3) (POTENTIAL).
C (M3) (POTENTIAL).
D (M4) (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
E (M5) (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
F (M5A) (POTENTIAL). EXTRACELLULAR (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

I (M7) (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

K (M9) (POTENTIAL).

EXTRACELLULAR (POTENTIAL). CYTOPLASMIC (POTENTIAL).
G (M5B) (POTENTIAL). CYTOPLASMIC (POTENTIAL) Sodium transport; Transport; (POTENTIAL) (POTENTIAL) Symport;

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Best Local S
Matches 148
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Q01345;
Q01345;
Q1346;
Q1347;
Q1347;
Q1347;
Q1347;
Q138, Created)
Q1-JUN-1994 (Rel. 29, Last sequence update)
Q1-JUN-1994 (Rel. 38, Last annotation update)
Q15-JUL-1999 (Rel. 38, Last annotation update)
Na(+)/H(+) exchanger beta (Na(+)/H(+) antiporter) (Beta (Na(+)/H(
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                             Borgese F., Sardet C., Cappadoro M., Pouyssegur J., Motais R.;

"Cloning and expression of a cAMP-activated Na+/H+ exchanger:

"Cloning and expression mediates hormonal regulation.";

Proc. Natl. Acad. Sci. U.S.A. 89:6765-6769(1992).

"I Proc. Natl. Acad. Sci. U.S.A. 89:6765-6769(1992).

"I PROC. NATION PROC. EXTRUDING SYSTEM DRIVEN BY THE INWARD CONDITIONS. MAJOR PROCON EXTRUDING SYSTEM DRIVEN BY THE INWARD
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                                                                                                                                                                                                                                                                                     TISSUE=Nucleated erythrocyte;
MEDLINE=92357712; PubMed=1379718;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGAETIIFMFLGISAVDPVIWTW------NTAFVLLTLVFISVYRAIGVVLQTWILNRY
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EXTRACELLULAR (POTENTIAL).

M (M10) (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTINIC CROSS)

N-TASPETODFF99E3F CRC64;
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PTM: ACTIVATED BY CAMP, PROTEIN KINASE A AND PROTEIN KINASE C
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PHOSPHORYLATION (BY CAPK) (POTENTIN
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N-LINKED (GLCNAC. . . ) (POTENTIAL)
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EMBL; M85299; AAA98479.1; -.
PIR; A40204; A40204.
InterPro; IPR000676; NaH_Exchngr.
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J. Biol. Chem. 267:9331-9339(1992).

J. Biol. Chem. 267:9331-9339(1992).

IF FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-SPRAGUE-DAWLEY; TISSUE-Heart;
MEDLINE-92250539; PubMed-1577762;
Orlowski J., Kandasamy R.A., Shull G.E.;
"Molecular cloning of putative members of the Na/H exchanger gene family, cDNA cloning, deduced amino acid sequence, and mRNA tissue expression of the rat Na/H exchanger NHE-1 and two structurally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAH1_RAT
P26431;
           Pfam; PF00999; Na_H_Exchanger; 1.
PRINTS; PR01084; NAHEXCHNGR.
Transmembrane; Glycoprotein; Sodium transport; Transport;
Multigene family; Phosphorylation.
DOMAIN
1 12
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                      use by non-profit institutions as long as modified and this statement is not removed. [
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sodium/hydrogen exchanger 1 (Na(+)/H(+) exchanger SLC9Al OR NHE1.
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01-OCT-1996 (Rel. 34, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: NOT TISSUE SPECIFIC.
PTM: PHOSPHORYLATED (POSSIBLE).
SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC
                                                                                                                                                                                                                                                                                                                                                                                 DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG CAUTION: HYDROPHOBIC DOMAINS A, B AND L ARE NOT TRANSMEMBRANAL, BUT ONLY MEMBRANE-ASSOCIATED.
                                                                                                                                                                                                                                                                                                  veen the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the Excurpean Bioinformatics Institute. There are no restrictly non-profit institutions as long as its content
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                                                                                                                                                                                                          s requires a license agreement (S an email to license@isb-sib.ch).
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         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.9%;
28.0%;
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E (M5) (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

F (M5A) (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

G (M5B) (POTENTIAL).

EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H (M6) (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

I (M7) (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

J (M8) (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

K (M9) (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
B (M2) HYDROPHOBIC.
CYTOPLASMIC (POTENTIAL).
C (M3) (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
D (M4) (POTENTIAL).
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Pred.
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N-LINKED (GLCNAC. . .) (P
; 58398DE74A9642FB CRC64;
                                                                                                                                                                                                     ---ETKRSINEEIHTQFLDH--
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      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          467.5; DB 1
No. 1.1e-22;
      822
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Gaps

20;

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DOMAIN
CARBOHYD
SEQUENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P48761;
01-FEB-1996 (Rel. 33,
01-FEB-1996 (Rel. 33,
15-JUL-1999 (Rel. 38,
                                                                                                                                                                                                                                             DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Counillon L., Pouyssegur J.;
"Nucleotide sequence of the Chinese hamster Na+/H+ exchanger NHE1.";
Biochin. Biophys. Acta 1172:343-345(1993).
-I- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Sodium/hydrogen exchanger 1 (Na(+)/H(+) excha
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DOMAIN
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLC9A1 OR NHE1.
                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93192332; PubMed=8383540;
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                                                                                                                                                                                                                                                                                                                           DOMAIN
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                                                   DOMAIN
                                                                                                                        TRANSMEM
                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                              Multigene
                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane;
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                                        TRANSMEM
                                                                                                                                                   TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Integral membrane protein.

PTM: PHOSPHORYLATED (POSSIBLE).

SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.

CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.

CAUTION: HYDROPHOBIC DOMAINS A, B AND L ARE NOT BELIEVED TO BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSMEMBRANAL, BUT ONLY MEMBRANE-ASSOCIATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSDUCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00999;
                                                                                                                                                                                                                                                                                                                                                                                              family;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Na_H_Exchanger;
                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                        NAHEXCHNGR
                                                                                                                                                                                                                                                                                                                                                                                               norylation
 ₩;
           L, HYDROPHOBIC:
EXTRACELLULAR (POTENTIAL).
M (M10) (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC...) (POT
                                                                                                                                                                                                                                                        C (M3) (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
D (M4) (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
E (M5) (POTENTIAL).
                                                                                                                                                                                                                                                                                                               B (M2) HYDROPHOBIC.
CYTOPLASMIC (POTENTIAL).
C (M3) (POTENTIAL).
                                                                             J (M8) (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
K (M9) (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                  EXTRACELLULAR (POTENTIAL)
H (M6) (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
I (M7) (POTENTIAL).
                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                          Sodium transport; Transport;
                                                                                                                        EXTRACELLULAR (POTENTIAL)
J (M8) (POTENTIAL).
                                                                                                                                                                                                                                  EXTRACELLULAR F (M5A) (POTE)
                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                 (M1) HYDROPHOBIC
                                                                                                                                                                                                                                (M5A) (POTENTIAL)
 E97C1ACD4EB88DAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exchanger
                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
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; Cricetinae;
              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             restrictions
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Best Local Similarity
Matches 144; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAH3_DIDMA
Q28362;
                                                                                                                                                                                                   Amemiya M., Yamaji Y., Cano A., Moe O.W., Alpern R.J.;
"Acid incubation increases NHE-3 mRNA abundance in OKP cells.";
Am. J. Physiol. 269:C126-C133(1995).
-i- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATED
BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD
SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Didelphis marsupialis virginiana (North American opossum).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIDMA
                                                                           -!- SUBCELLULAR LOCATION: Integral
-!- PTM: PHOSPHORYLATED (POSSIBLE)
-!- SIMILARITY: BELONGS TO THE NA!
-!- CAUTION: THE NUMBER, LOCALIZAT!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=95358256; PubMed=7631739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLC9A3 OR NHE3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sodium/hydrogen exchanger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9267;
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                                              PTM: PHOSPHORYLATED (POSSIBLE).
SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
SAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF H
DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS
                                                                                                                                                                                  TRANSDUCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MLMSYLSYIMAELFYLSGILTVFFCGIVMSHYTWHNVTESSRVTTRHSFATLSFVAETFI
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  SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLMTKPLINLLLPPHKQMPSGHSSMTTSEPSSPKHFTVPLLDNQPDSESDMITGPEVARP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TALRMLLRTPTHTVHRYWR----KFDDSFMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDKISFRQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMITSTVTVVLFSTVVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLYSYMAYLSAELFHLSGIMALIASGVVMRPYVEANISHKSHTTIKYFLKMWSSVSETLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FFLFLLPPIILDAGYFLPLRQFTENLGTILIFAVVGTLWNAFFLGGLLYAVCLVGGEQIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 35, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -DICGHYGHHHWKDKLNRFNKKYVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Pfam; PF00999;
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                 YRMVQLEIIDQVVMSYGGL-RGAVAYALV----VLLDEKKVKEKNLFVSTTIIVVFFTVI
                                                                                                                                                     EVALMMLMSYLSYIMAELFYLSGILTVFFCGIVMSHYTWHNVTESSRVTTRHSFATLSFV
                                 NSSDKISFRQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMITSTVTVVLFSTV
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M10 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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M5A (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

M5B (POTENTIAL).

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M6 (POTENTIAL).
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EXTRACELLULAR (I M2 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
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M8 (POTENTIAL).
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Brant S.R., Yun C.H., Donowitz M.,
"Cloning, tissue distribution, and
"Cloning, tissue distribution, and
Na+/N+ exchanger isoform, NHE3.";
Am. J. Physiol. 269:C198-C206(1995)
-i- FUNCTION: INVOLVED IN PH REGULA
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 cortex;
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CYTOPLASMIC (POTENTIAL).
E (M5)
                                                                               CYTOPLASMIC (POTENTIAL).
G (M5B) (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
C (M3) (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
I (M7) (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
J (M8) (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                     H (M6) (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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(POTENTIAL).

(POTENTIAL)

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01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Sodium/hydrogen exchanger 3 (Na(+)/H(+) exchanger 3) (NHE-3).
entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Electropean Bioinformatics Institute. There are no restricted the state of the s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Integral membrane protein.

PTM: PHOSPHORYLATED (POSSIBLE).

SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.

CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HY

DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
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BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE
SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN
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                                                                                                                              and this statement is not removed.
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SOFFITTI

TRANSMEM DOMAIN DOMAIN DOMAIN

K (M9) (POTENTIAL) EXTRACELLULAR (POT

(POTENTIAL)

INWARD

SIGNAL

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LLC-PK1 renal Am. J. Physiol -!- FUNCTION:
                                                   SEQUENCE FROM N.A.
MEDLINE=92087905; PubMed=
Reilly R.F., Hildebrandt
Pouyssegur J., Aronson P.
                                                                                                                                                                  NAH1_PIG STANDARD; PRT; 818 AA. P48762; O1-FEB-1996 (Rel. 33, Created) O1-FEB-1996 (Rel. 33, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Sodium/hydrogen exchanger 1 (Na(+)/H(+) exchanger 1 OR NHEI. Sus scrofa (Pig).
          MEDLINE=92087905; PubMed=1661081;
Reilly R.F., Hildebrandt F., Biemesderfer D., Sardet Reilly R.F., Hildebrandt F., Biemesderfer D., Sardet Pouyssegur J., Aronson P.S., Slayman C.W., Igarashi F. Pouyssegur J., Aronson P.S., Stayman C.W., Igarashi F. "CDNA cloning and immunolocalization of a Na(+)-H+ ex LLC-FK1 renal epithelial cells.";
Am. J. Physiol 261:F1088-F1094(1991).
                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                          NCBI_TaxID=9823;
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N-LINKED (GLCNAC. . .) (P
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EXTRACELLULAR (POTENTIAL).

M (M10) (POTENTIAL).

CYTOPLASMIC (POTENTIAL).
REGULATION TO ELIMINATE ACIDS GENERATED
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2.8e-22;
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DOMAIN
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EMBL; S71135; AAB20633.1; -.
InterPro; IPR000676; NaH_Exchngr.
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PTM: PHOSPHORYLATED (POSSIBLE).

SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.

CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYI

DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.

CAUTION: HYDROPHOBIC DOMAINS A, B AND L ARE NOT BELIEVED
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een the Swiss Institute of Bioinformatics and
NIGLLDNLLFGSIISAVDFVAVLAVFEEIHINELLHILVFGESLLNDAVTVVLYHLFEEF
                                                                         FFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTLISCSIIS--FGAVKIFKHLDID
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                      FLDFGDYLAIGAIFAATDSVCTLQVLSQDE-TPLLYSLVFGEGVVNDATSVVLFNAIQSF
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B; Mismatches
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CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (
H -> Y (IN REF. 1; AAB20
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J (M8) (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENT
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D (M4) (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
C (M3) (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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DENOMINATION OF HYDROPHOBIC
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CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tse C.-M., Ma A.I., Yang V.W., Watson A.J.M., Levine S., Montrose M.H., Potter J., Sardet C., Pouyssegur J., Donowitz Molecular cloning and expression of a cDNA encoding the rabb. Villus cell basolateral membrane Na+/H+ exchanger."; EMBO J. 10:1957-1967(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P23791;
01-NOV-1991
01-NOV-1991
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MEDLINE=92096447; PubMed=1661611;
                                                                                                                                                                                                                           exchanger."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-NEW ZEALAND WHITE; TISSUE-Ileal villus; MEDLINE-91293066; PubMed-1712287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Ci
Mammalia; Eutheria; Lagomorpha;
                                                                                                                                                                                                                                                                           Fliegel
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01-NOV-1991 (Rel.
30-MAY-2000 (Rel.
                                                                                                                                                                                                                                                  "Identification
                                                                                                                                                                                                                                                                                               MEDLINE-91138752; PubMed-1704856;
                                                                                                                                                                                                                                                                                                                           STRAIN-NEW ZEALAND WHITE;
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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SUBCELLULAR LOCATION: Integral TISSUE SPECIFICITY: KIDNEY AND PTM: PHOSPHORYLATED (POSSIBLE)
                                                                                         3 LETT. 279:25-29(1991).
FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GENERATI ETUNCTION: HETABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE INWARD SODIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN SIGNAL
                                                                                 TRANSDUCTION
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Chordata; Craniata; Vertebrata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYDROPHOBIC DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    European Bioinformatics Institute.
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$16328; $16328.
                                     MNLFVALLCACIVLGHLLEE · NRWVNESITALIIGLCTGVVILLLSGGKSSHLLVFSEDL 83
-- ANYDHYGIVDIVLGFL-SFFVVALGGVFVGVVYGVIAAFTSR---
                DMTSFD----PKIGLHFIGNFLYLFLSSTFLGVGIGLLCAYIIKKLYFGRHSTDREVALM
                                                                          FFLFLLPPIILDAGYFLPLRQFTENLGTILIFAVVGTLWNAFFLGGLMYAVCLVGGEQIN
                                                                                             FFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTLISCSIIS--FGAVKIFKHLDID 141
                                                                                                               ISLWILLACLMKIGFHVIPTISSIVPESCLLIVVGLLVGGLIKGV-GEKPPFL---QSEV 160
                                                                                                                                                        144;
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Pred. No. 3.
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N-LINKED (GLCNAC. )
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-> E (IN REF. 2).
336738D267F7F436
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В	Qy	Ъ	Qy	рь	Qy	В	Qy	DЪ	Qy
536DICGHYGHHWKDKLNRFNKKYVK 559	494 TALRMLLRTPTHTVHRYWRKFDDSFMR 520	496 GMTIRPLYDLLAVKKKQETKRSINEEIHTQFLDHLLTGIE 535	MPSGHSSMTTSEPSSPKHFTVPLLDNQPDSESI	441 IVKLTPKDQFIIAYGGL-RGAIAFSLGYLLDKKHEPMCDLFLTAIITVIFFTVFVQ 495	374 SDKISERQQIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMITSTVTVVLESTVVF 433	395 FIFLGVSTVAGSHHWNWTFVISTLLFCLIARVLGVLGLTWFINKFR 440	317 FLYVGMDALDIEKWKFVKNSQGLSVAVSSILVGLILVGRAAFVFPLSFLSNLAKKNS 373	335 FLYSYMAYLSAELFHLSGIMALIASGVVMRPYVEANISHKSHTTIKYFLKMWSSVSETLI 394	257 MLMSYLSYIMAELFYLSGILTVFFCGIVMSHYTWHNVTESSRVTTRHSFATLSFVAETFI 316

Search completed: October 18, 2002, 12:26:10 Job time : 19 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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Perfect score:
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      Issued_Patents_AA:*

1: /cgn2_6/ptodata/1

2: /cgn2_6/ptodata/1

3: /cgn2_6/ptodata/1

4: /cgn2_6/ptodata/1

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6: /cgn2_6/ptodata/1
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/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
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US-08-677-734A-10
US-08-677-049-9
US-09-013-053-2
US-09-014-969-11
US-08-928-692-13
US-08-466-343D-2
US-09-087-232A-13
US-08-88-61100-14
US-08-896-1100-2
US-09-144-914-8
US-08-141-2
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US-08-08-141-2
US-09-097-889-15
US-08-098-768-2
US-09-097-759-3
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US-08-8800-291B-6
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US-08-677-734A-12
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GENERAL INFORMATION:
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4 US-09-045 4 US-09-037 2 US-08-225 2 US-08-225 2 US-08-29 2 US-08-99 2 US-08-91 3 US-09-195 1 US-09-045 4 US-09-066 4 US-09-05 4 US-09-328 4 US-09-328 4 US-09-328 4 US-09-328 6 US-09-328 7 US-09-328 8 US-09-328 9 US-09-328
US-09-045-583-58 US-08-672-814D-2 US-09-333-696-2 US-09-097-759-4 US-09-097-759-4 US-09-097-759-4 US-09-195-391-4 US-09-195-391-4 US-09-195-391-4 US-09-0461-244-2 US-09-046-047-7 US-09-066-047-7 US-09-08-593-12 US-09-238-930-2 US-09-328-320-2 US-09-328-320-2 US-09-328-320-2 US-09-336-080-6 US-08-800-2918-5 US-09-097-889-22

ALIGNMENTS

INFORMATION:

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INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 832 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-677-734A-12
                    Query Match
Best Local
    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                   TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: FOIGLS, Jean B.
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05
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CITY: Washington
STATE: D.C.
    Local Similarity tes 147; Conserv
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1300 I Street, N.W., Suite 700
    Conservative
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17.0%; Score 471.5;
28.4%; Pred. No. 3.66
tive 92; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Funct: TITLE OF INVENTION: NHE3.
                 NAME: Fordis Jean B.
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05387.0043-00000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tse, Chi
TITLE OF INVENTION:
                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                      STATE: D.C
                                                                                                                                                                                                                                                                                                                                       CITY: Washington
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TELEPHONE:
                                                                                                                              FILING DATE: 10-JUL-1996
                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Finnegan, Henderson, Farabow, ADDRESSEE: Dunner
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(202)
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                                                                                                                                                                                                                                                                                                                                                         Suite 700
                                                                                                                                                                                        #
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RESULT 3
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Best Local Similarity
Matches 146; Conserv
                                                                                                                                                                                                                                                                                                    Sequence 9, Application Patent No. 5871919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202) 408-4400 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                              APPLICANT: Brant, Steven R.
APPLICANT: Yun, Chris C.H.
APPLICANT: Donowitz, Mark
APPLICANT: Tse, Chung-Ming
TITLE OF INVENTION: Cloning, Tissue Distribution, and
TITLE OF INVENTION: Punctional Analysis Of The Human
TITLE OF INVENTION: NHE3.
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         479
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             COUNTRY: USA
ZIP: 20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 VVSMNLFVALLCACIV-LGHLLEENRWVNESITALIIGLCTGVVILLLSGGKSSHLLVF- 79
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                                                STATE:
                                                              CITY: Washington
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                                                                                E: Dunner
1300 I Street,
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linear
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27.7%;
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Pred. No. 7.2e-38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -KVKRSEQREPKLNEKLHGRAFDHILSAIED---
                                                                                 Suite
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                                                 Sequence 10, Application US/08677734A Patent No. 5871919
GENERAL INFORMATION:
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Best Local Similarity 28.6
Conservative
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                APPLICANT:
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LENGTH: 834 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 408-4000
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            311 AITFCGICCQKYVKANISEQSATTVRYTMKMLASSAETIIFMFLGISAVNPFIWTW----
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STRANDEDNESS: single
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                KFDDSFMRPV 522
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                                                                                                                                                                             HFDRKFLSRV
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                                                                                                                                                                                                                                                                                                                  FALV----VLLDGDKVKEKNLFVSTTIIVVFFTVIFQGLTIKPLVQWL----KVKRSEHR
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                Brant, Steven R. Yun, Chris C.H.
Donowitz, Mark
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Pred. No. 4e-37;
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Best Local Similarity
Matches 140; Conserv
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INFORMATION FOR SEQ ID NO:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Fordis, Jean B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: Cloning, Tissue Distribution, and
TITLE OF INVENTION: Functional Analysis Of The Human Na+/H+ Exchanger Isoform,
TITLE OF INVENTION: NHE3.
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                          367 ---NTAFVLLTLVFISVYRAIGVVLQTWLLNRYRMVQLEPI---DQVVLSYGGL-RGAVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/0 FILING DATE: 10-JUL-1996 CLASSIFICATION: 435
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                SMTTSEPSSPKHFTVPLLDNQPDSESDMITGPEVARPTALRMLLRTPTHTVHRY----WR
                                                                    FALV----VLLDGDKVKEKNLFVSTTIIVVFFTVIFQGLTIKPLVQWL----KVKRSEHR
                                                                                                        IALAYNKFTTSGHTSLHENAIMITSTVTVVLFSTVVFGLMTKPLINLLLPPHKQMPSGHS
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                                                                                                                                                                                                                                                                                        FFVVSLGGTLVGVVFAFLLSLVTR---FTKHVRIIEPGFVFIISYLSYLTSEMLSLSAIL
                                                                                                                                                                                                                                                                                                                          FLYLFLSSTFLGVGIGLLCAYIIKKLYFGRHSTDREVALMMLMSYLSYIMAELFYLSGIL 276
                                                                                                                                                                                                                                                                                                                                                                                                                                    FGNLGTILLYAVVGTVWNAATTGLSLYGVFLSGLMGDLQIGLLDF---LLFGSLMAAVDP 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FVNFMTIMLFGAIGTLISCSIISFGAVKIF-----KHLDIDFLDFGDYLAIGAIFAATDS 160
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1300 I Street,
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NO: 10:
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US-08-677-049-9
                                                                                                        US-08-677-049-9
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                                        Query Match
Best Local Similarity
Matches 103; Conserv
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,788
FILING DATE: 03-JUL-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Zlotnik, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 415-852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                  FEATURE:
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                                                                                                                                                                                                 NAME/KEY: Region LOCATION: 323..357 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                            NAME/KEY: Region
LOCATION: 115..144
OTHER INFORMATION: /
OTHER INFORMATION: 4
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                                                                                                                                                    NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                           NAME/KEY:
LOCATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 901 California Avenue CITY: Palo Alto
STATE: California
   56 IIGLCTGVVILLLSGGKSSHLLVFSEDLFFIYLLPPIIFNAG----FQVKKKQFFVNFMT 111
                                                                                                                     OTHER INFORMATION: OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
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Bazan, J. Fernando
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359..386
                                           Conservative
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                                        Score 112.5; DB 2;
Pred. No. 0.0076;
9; Mismatches 153;
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; LENGTH: 1394
; TYPE: PRT
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Best Local S
Matches 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: CANINE HERPESVIRUS BASED RECOMBINANT TITLE OF INVENTION: PARTICULAR AGAINST CANINE DISTEMPER, TITLE OF INVENTION: PARAINFLUENZA 2 VIRUS FILE REFERENCE: 454313-2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/213,053
CURRENT FILLING DATE: 1998-12-16
EARLIER APPLICATION NUMBER: 9608242
EARLIER FILLING DATE: 1996-06-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: AUDONNET, Jean-Christophe APPLICANT: BAUDU, Philippe
                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 31
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EARLIER FILING DATE: 1997-06-23
                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.1
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hes 114; Conserv
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                        IISFGAVKIFKHLDIDFLDFGDYLAIGAIFAATDSVCTLQVLSQDETPLLYSLVFGEGV- 184
                                                                                                                                                                                           SVVSMNLFVALLCACIVLGHLLEENRWVNESITALIIGLCTGVVILLLS------GGKSS
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                                                                            SICRISQSIFVTIAAFCWGFDWILNPI
                                                                                                            HLLVFSEDLF------FIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTLISCS 125
--AIKIILILSLSFL---
                                                                                                                                                                                                                               4.0%; Score 109.5; DB 4; ilarity 20.4%; Pred. No. 0.087; Conservative 84; Mismatches 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -SDKISFRQQII--IWWAGLMRGAVSIALAYN-KFTTSGHTSLHEN 415
    -----TICTIKI----HIFYLISILNGSGSH 577
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US-09-014-969-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                              TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 635 amino acids
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/014,969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Spaulding, Vikki
APPLICANT: Agostino, Michael J.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
                                                                                                                        TELEPHONE: (617) 498-8284
                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sprunger, Suzanne
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
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                                                                                                                      TELEPHONE:
                                                                                                                                                             NAME: Sprunger, Suzanne A. REGISTRATION NUMBER: 41,323
                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A. ZIP: 02140
TOPOLOGY: 11
                                  TYPE: amino acid
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87 CambridgePark Drive
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LaVallie, Edward R.
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linear
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RESULT 8
US-08-714-070A-1
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                                                                                                                                                                                                                                                                                                                  Patent No. 5834237
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 106; Conserv
                                                                                                                                                                                                                                                                                                                                                  Sequence 1,
             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE,
                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                     CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1444
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APPLICATION NUMBER:
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P.O. Box 1404
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SILVESTRE, Nath
SCHWEINBRYBER,
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nilarity 19.3%;
Conservative 83
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US/08/714,070A
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RESULT 9
US-08-928-692-13
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                                                                                                                                                                                               Sequence 13, Application US/08928692 Patent No. 5958727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94/01767
FILING DATE: 10-MAR-1994
ATTORNEY/AGENT INFORMATION:
                  NUMBER OF SEQUENCES: 80

CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59587270 No. 5958727disk of No.
                                                                  APPLICANT: Hansen, Kim
TITLE OF INVENTION: Methods for METITLE OF INVENTION: a Polypeptide
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LENGTH: 775 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 836-6620
                                                                                                                             APPLICANT:
                                                                                                                                               APPLICANT:
                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             171 ISFRDQLKVGKLEDTLYLGPTTSEAFIERLQNELELESISEDDLYSKRLSPSVSYSEFDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 GVVNDATSVVLFNAIQSFDMTSFDPKIGL------HFIGNFLYLFLSSTFLGVGIGLLC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 LDFGDYLAIG------AIFAATDSVCTLQVLSQDE-----TPLLYSLVFGE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296 SSRVTTRHSFATLSFVAETFIFLYVGMD-----ALDIEK------W-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 30,427
REFERENCE/DOCKET NUMBER: 017753-077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Rea, Teresa Stanek REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                              DSLYWNPSPSFESQVNSVRRIYARLELWKSDLHSSVVFDESAVQHPLFRSNAHVQMIYDN
                                                                                                                                                                                                                                                                                                                                                                                                             DKI-----SFRQQI-----IIWWAGLMRGAV--SIALAYNKFTTSGHTS-LHEN 415
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 405 Lexington Avenue
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Lamsa, Michael
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19.9%;
                                                                                        Methods for Modifying
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                                                                                          the Production
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                      5958727th America, Inc.
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RESULT 10
US-08-466-343D-2
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                                  Sequence 2, Application Patent No. 6025154
GENERAL INFORMATION:
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Matches 89; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 49
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
APPLICANT: LI, Yi
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: 11
MOLECULE TYPE:
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NAME: Lambiris, Elias J
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                                                                                                                                                                 439 GFSSWG-----IVIIVFIIVFAAFYALGIGTVPWQQSELFPQNVRGIGTSYATAT 488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM CONTROL OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 SSHLLVFSEDLF-FIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTLISCSIISFGA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 12-SEP CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----DLDHKYLTYGEKEIVTAATSLGALITSIFAGTAADIFGRKRCLMGSNLMFVIGAI 171
                                                                                                                                                                                                                                                                                                                                                                                                                          SFATLSFVAETFIFLYVGMD---ALDIEK------
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                                                                                                                                                                                                                                                                                                                                              ---WKFVKNSQGLSVAVSSILVGLILVGRAAFV-----FPLSFLSNLAKKNSS----
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                                                                        US/08466343E
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 POLYNUCLEOTIDES ENCODING HUMAN G-PROTEIN
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                                                                                                                                                       RESULT 11
US-09-087-232A-13
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                                                                                   Sequence 13, Application US/09087232A Patent No. 6153431
GENERAL INFORMATION:
APPLICANT: Quillent et al.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1150000/EKS/KLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/466,343D
FILING DATE: 06-JUN-1995
                                                 APPLICANT: Quillent et al.
TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS CO-RECEPTOR
TITLE OF INVENTION: VARIANTS ASSOCIATED WITH RESISTANCE TO VIRUS INFECTION
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MEDIUM TYPE: Floppy
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NUMBER OF SEQUENCES:
                 NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                143 TF--GVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSH-FPY------SQYQFWK 191
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                                                                                                                                                                                                                                                                                              250 ---PYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 PPLYSLVFIFGFVGNMLVILILINCQRLESMTDI------YLLNLAISDLFFLLTV 83
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   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                            MRGAVSIALAYNKF-----TTSGHTSLHENAIMITST--VTVVLFSTVVFGLMTKPLIN 442
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                                                                                                                                                                                                                                                                                                                                                                                            NSQGLSVAVSSILVGLI--LVGRAAFVFPLSFLSNLAKKNSSDKISFRQQII--IWWAGL 390
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Baker & Botts, L.L.P. attn. Lisa Kole
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Pred. No. 0.
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NW, SUITE 600
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RESULT 12
US-08-861-105-14
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
TYPE: amino acids
                                                                                                                                                                                 Patent No.
                                                                                                                                                                                    Sequence 14, Application US/08861105 Patent No. 6258527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                            GENERAL INFORMATION:
APPLICANT: LITTMAN, DAN R.
APPLICANT: LITTMAN, DONGKUI
APPLICANT: ELLMEIER, WILFRIED
APPLICANT: LANDAU, NATHANIEL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 30 MAY 1997
ATTORNEY/AGENT INFORMATION:
NAME: KOLE, LISA B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 28 MAY 19
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APPLICATION NUMBER: 60/048,057
FILING DATE: 30 MAY 1997
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MEDIUM TYPE: Floppy disk
APPLICANT: LANDAU, NATHANIEL R.
APPLICANT: LIU, RONG
TITLE OF INVENTION: G-COUPLED RECEPTORS ASSOCIATED WITH
TITLE OF INVENTION: MACROPHAGE-TROPHIC HIV, AND DIAGNOSTIC AND THERAPEUTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 408-2628
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           335 NSQGLSVAVSSILVGLI--LVGRAAFVFPLSFLSNLAKKNSSDKISFRQQII--IWWAGL 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 35,225 REFERENCE/DOCKET NUMBER: AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 PFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLAVVHA-VFALKARTV
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66; Conserv
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Pred. No. 0.17;
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REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
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INFORMATION FOR SEQ ID NO: 14:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,105
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LENGTH: 352 amino acids
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CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/666,020
FILING DATE: 19-JUN-1996
CLASSIFICATION: 436
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APPLICATION NUMBER: US 08/227,319
FILING DATE: 13-APR-1994
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NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                            143 TF--GVVTSVITWVVAVFASLPGIIFTRSQKEGLHYTCSSH-FPY------SQYQFWK 191
                                                                                                                                                            192 NFQTLKIVILGLVLPLLVMVICYSGILKTLLRCRNEKKRHRAVRLIFTIMIVYFLFWA---
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307 YLL 309
                                    443 LLL 445
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                                                                              250 ---PYNIVLLLNTFQEFFGLNNCSSSNRLDQAMQVTETLGMTHCCINPIIYAFVGEKFRN
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STREET: 411 Hackensack Ave, Continental Plaza,
STREET: Floor
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                 84 PFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLAVVHA-VFALKARTV 142
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TOPOLOGY: line
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RESULT 14

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RESULT 15
US-09-268-140-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (617)227-7.
TELEFAX: (617)742-421.
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 352 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (617)227-7400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Graham, Gerard J. et al.
TITLE OF INVENTION: No. 6287805el Molecules of the G Protein-Coupled
NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 PLLYSLYFGEGVV-NDATSVVLFNAIQSFDMTSFDPKIGLHFIGNFLYLFLSSTFLGVGI 231
                                                                                                       443
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                              84 PFWAHYAAAQWDFGNTMCQLLTGLYFIGFFSGIFFIILLTIDRYLAIVHA-VFALKARTV 142
                                                                                                                                                                                                                                                                                                                                                                                                               34 PPLYSLVFIFGEVGNMLVILILINCKRLKSMTDI-----YLLNLAISDLFFLLTV 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/045,583 FILING DATE: 20-MAR-98
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                                                                     YLL 309
                                                                                                                                                                   MRGAVSIALAYNKF----TTSGHTSLHENAIMITST--VTVVLFSTVVFGLMTKPLIN 442
                                                                                                                                                                                                                                    NSQGLSVAVSSILVGLI--LVGRAAFVFPLSFLSNLAKKNSSDKISFRQQII--IWWAGL 390
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APPLICANT: Drabkin, Harry A.
APPLICANT: Drabkin, Harry A.
APPLICANT: Drabkin, Harry A.
TITLE OF INVENTION: TRC8, A GENE RELATED TO THE HEDGEHOG RECEPTOR, PATCHED FILE REFERENCE: 93445-00004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/268,140 CURRENT FILING DATE: 2000-03-12 PRIOR APPLICATION NUMBER: US 60/077,723 PRIOR FILING DATE: 1998-03-12
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                                              371 KNSSDKISFRQQIIIWWAGLMRGAVSI--------ALAYNKFTTS 407
                                                                                         456 KLDDYVYYVRSTG---SIIEFIFGVVMFGNGAYTMMFESGSKIRAFMMCLHAYFNIYLQA 512
                                                                                                                                       326 DIEKWKFVKNSQGLSVAVSSILVGLILVGRAAFVFPLS---
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WKTFMNRRTAVKKINSLPEIKGSRLQEINDVCAICYHEFTTS
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Search completed: October 18, 2002, 12:24:38 Job time: 19 secs

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Result
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DT (01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
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MEDLINB=21276661; PubMed=11382810;

MEDLINB=21276661; PubMed=11382810;

Yamaguchi T., Fukada-Tanaka S., Inagaki Y., Saito N.,

Yonekura-Sakakibara K., Tanaka Y., Kusumi T., Iida S.

"Genes Encoding the Vacuolar Na+/H+ Exchanger and Flov

"Benat Cell Physiol. 42:451-461(2001).

EMBL; AB054979; BAB60901.1; -

EMBL; AB054979; BAB60901.1; -

SEQUENCE 542 AA; 60024 MW; 0C8381CFB78B239C CRC64
                                                                                                                                                                                                                                                                                                                           Ipomoea tricolor (Morning glory).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

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Query Match
Best Local
                                                             halophyte Atriplex gmelini.";
plant Mol. Biol. 46:35-42(2001).
EMBL; AB038492; BAB11940.1;
InterPro; IPR001179; FKBP_PPTase.
InterPro; IPR000676; NaH_Exchngr.
Pfan; PF00999; Na, H_Exchanger; 1.
PRINTS; PR01084; NAHEXCHNGR.
PROSITE; PS00453; FKBP_PPTASE_1; UN
SEQUENCE 555 AA; 61504 MW; ACD5
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Q1-MAR-2001 (TrEMBLrel. 1
Q1-MAR-2001 (TrEMBLrel. 1
Q1-DEC-2001 (TrEMBLrel. 1
NA/H ANTIPORTER NHX1.
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Atriplex gmelini.
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyllidae; Caryophyllales; Chenopodiaceae; Atriplex.
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=21330247; Hamada A., Shono M
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Q94LX4;
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NA H-ANTIPORTOR.
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Submitted (NOV-2000) to
EMBL; AB051818; BAB5610
SEQUENCE 553 AA; 611
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nierembergia.
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Tida S., Kusumi T., Yonekura-Sakakibara K., Tanaka Y.;

"Plant Na-H antiportor.";

Submitted (NOY-200) to the EMBL/GenBank/DDBJ databases

EMBL; AB051817; BAB56105.1;

SEQUENCE 540 AA; 59510 MW; BCE2740F275E896A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Petunia hybrida (Petunia).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo Eukaryota; Viridiplantae; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Petunia.

NCBI_TaxID=4102;
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Best Local S
Matches 407
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Submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY028416; AAK27314.2; .
SEQUENCE 542 AA; 59836 MW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Citrus paradisi (Grapefruit).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Sapindales; Rutaceae; Citrus.

NCBI_TaxID=37656;
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D1-JUN-2001 (TrEMBLrel. 17,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
SODIUM/PROTON EXCHANGER.
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                      SFATLSFVAETFIFLYVGMDALDIEKWKFVKNSQGLSVAVSSILVGLILVGRAAFVFPLS
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                                                                                              FGRHSTDREVALMMLMSYLSYIMAELFYLSGILTVFFCGIVMSHYTWHNVTESSRVTTRH
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Pred. No. 1.8
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01-DEC-2001
01-DEC-2001
01-DEC-2001
NA+/H+ ANTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhang H., Zhang Q., Ma X.;
"Na+/H+ antiporter in Suaeda salsa.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AF370358; AAK53432.1;
SEQUENCE 556 AA; 61672 MW; DDF6AB696647D48E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suaeda maritima subsp. salsa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachec Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Chenopodiaceae; Suaeda.
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-VARPTALRMLLRTPTHTVHRYWRKFDDSFMRPVFGGRGFVPFVAGSPVEQS
                                                         MTKPLINLLLPPHKQMPSGHSSMTTSEPSSPKHFTVPLLDNQPDSESDMITGPE----
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1.4e-150;
nes 62;
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Q9SXJ8;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2001
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Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.
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Pfam; PF00999; Na_H_Exchanger; 1.
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MEDLINE=99326147; PubMed=10395929;
Fukuda A., Nakamura A., Tanaka Y.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OSNHX1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR01084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular cloning and expression of the Na+/H+
                                                                       487
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                                                                                             LRMLLRTPTHTVHRYWRKFDDSFMRPVFGGRGFVPFVAGSPVEQS
                                                                                                                                                                                              MTKPLINLLLPPHKQMPSGHSSMTTSEPSSPKHFTVPLLDNQPDSESDMITGPEVARPTA
                                                                                                                                                                                                                                                        KISFRQOIIIWWAGLMRGAVSIALAYNKFTTSGHTSLHENAIMITSTVTVVLFSTVVFGL 435
||::|||:||||:||||||||:||:
KITWRQQVVIWWAGLMRGAVSIALAYNKFTRSGHTQLHGNAIMITSTITVVLFSTMVFGM 435
                                                                                                                                                                                                                                                                                                                                                         IFLYVGMDALDIEKWKFVKNSQGLSVAVSSILVGLILVGRAAFVFPLSFLSNLAKKNSSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MMLMSYLSYIMAELFYLSGILTVFFCGIVMSHYTWHNVTESSRVTTRHSFATLSFVAETF 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AIQSFDMTSFDPKIGLHFIGNFLYLFLSSTFLGVGIGLLCAYIIKKLYFGRHSTDREVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KHLDIDFLDFGDYLAIGAIFAATDSVCTLQVLSQDETPLLYSLVFGEGVVNDATSVVLFN 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLVFSEDLFFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTLISCSIISFGAVKIF 135
                                                                 LRMLLTKPTHTVHYYWRKFDDALMRPMFGGRGFVPFSPGSPTEQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MMLMAYLSYMLAELLDLSGILTVFFCGIVMSHYTWHNVTESSRVTTKHAFATLSFIAETF
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                                                                                                                                                                       MTKPLIRLLLP----
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AB021878; BAA83337.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             535 AA; 59070 MW; 6BCADDB29B131976 CRC64;
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                                                                                                                                                             ASGHP--VTSEPSSPKSLHSPLLTSMQGSDLESTT--NIVRPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49;
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Pred. No. 2.4
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RX MEDLINE-21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,
RA Fartmann B., Valle G., Bloecker H., Perzer-Alonso M., Obermaler B.,
RA Fartmann B., Valle G., Bloecker H., Perzer-Alonso M., Obermaler B.,
RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Pallavicini A., Toppo S., Simionati B.,
RA Wincker A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
RA Wincker D., Schoef M., Bangues M., Terol J., Climent J.,
RA Reichelt J., Scharfe M., Schoen G., Bargues M., Terol J., Climent J.,
RA Reichelt J., Scharfe M., Schoen G., Bargues M., Terol J., Chemin D.,
RA Reichelt J., Scharfe M., Berger-Llauro C., Purnelle B., Masuy D.,
RA Reichelt J., Scharfe M., Berger-Llauro C., Purnelle B., Masuy D.,
RA Monfort A., Argiriou A., Flores M., Liquori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mannhaupt G., Walts A., Utterback T., Fujil C., Shea T.P.,
RA Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Pai G., Militscher J., Sellers P., Gill J.E., Feldblym T.V.,
RA Kiyokawa C., Kohara M., Matsunoto M., Matsuno A., Muraki A.,
RA Watsha A., Yasuda M., Yasuda M., Tab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 408:820-822(2000).
EMBL; AC009465; AA651408.1; ...
InterPro; IPR001179; FKBP_PPlase.
InterPro; IPR000676; NaH_Exchanger; 1.
Pfam; PF00999; Na_H_Exchanger; 1.
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
PUTATIVE SODIUM PROTON EXCHANGER.
T9J14.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO1084; NAHEXCHNGR.
PROSITE; PS00453; FKBP_PPIASE_1;
SEQUENCE 546 AA; 60522 MW; BI
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid

eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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AIQSFDMTSFDPKIGLHFIGNFLYLFLSSTFLGVGIGLLCAYIIKKLYFGRHSTDREVAL
                                                                                                                                     KKLDIGTFDLGDFLAIGAIFAATDSVCTLQVLNQDETPLLYSLVFGEGVVNDATSVVLFN
                                                                                                                                                                         KHLDIDFLDFGDYLAIGAIFAATDSVCTLQVLSQDETPLLYSLVFGEGVVNDATSVVLFN
                                                                                                                                                                                                                                                                    LLVESEDLEFIYLLPPIIFNAGFQVKKKQFFRNFVTIMAFGAIGTVVSCTIISLGAIQFF
                                                                                                                                                                                                                                                                                                       LLVESEDLFETYLLPPITENAGEQVKKKQFEVNEMTIMLFGATGTLISCSITSFGAVKTE 135
                                                                                                                                                                                                                                                                                                                                                                                                       TSDHASYVSLNLFVALLCACIVIGHLLEENRMMNESITALLIGLGTGVVILLISRGKNSH 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TSDHASVVSMNLFVALLCACIVLGHLLEENRWVNESITALIIGLCTGVVILLLSGGKSSH
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Pred. No. 3e-1
56; Mismatches
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Best I
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STRAIN-CV. COLUMBIA;
STRAIN-CV. COLUMBIA;
MEDLINE-99145575; PubMed-9990049;
MEDLINE-99145575; PubMed-9990049;
Gaxiola R.A., Rao R., Sherman A., Grisafi P., Alper S.L.,
"The Arabidopsis thaliana proton transporters, AtNhxl and
"The Arabidopsis thaliana proton in yeast.";
function in cation detoxification in yeast.";
function in cation detoxification in yeast.";
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eueurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-MAY-1999 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
SODIUM PROTON EXCHANGER
                                                                                                                                                                                                                                                                                                                                                                                                                                               "The AtNHE1 gene encodes a putati
Submitted (MAR-1998) to the EMBL/
EMBL; AF106324; AAD16946.1; -.
EMBL; AF056190; AAF21755.1; -.
InterPro; IPR001179; FKBB_PPIase.
InterPro; IPR000676; NaH_Exchngr.
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prINTS; pr01084; NAHEXCHNGR.
prOSITE; pS00453; fKBP_ppIASE_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                  NON.
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                                                                                                                                                                               LSSLLQN-SDLFTSDHASVVSMNLFVALLCACIVLGHLLEENRWVNESITALIIGLCTGV
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                             CSIISFGAVKIFKHLDIDFLDFGDYLAIGAIFAATDSVCTLQVLSQDETPLLYSLVFGEG
                                                                      VILLLSGGKSSHLLVFSEDLFFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIGTLIS
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LDSLYSKLPSLSTSDHASYVALNLFVALLCACIVLGHLLEENRWMNESITALLIGLGTGV
                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                           538 AA;
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                                                                                                                                                                                                                                                      Conservative
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73.8%;
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10,
17, 1
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putative Na+/H+ antiporter.";
e EMBL/GenBank/DDBJ databases.
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Last sequence update)
Last annotation update)
1 (FRAGMENT).
                                                                                                                                                                                                                                                                           Score 2041;
Pred. No. 3.
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3.1e-148;
hes 71;
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Best Local
Matches 38
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Q94LX3;
01-DEC-2001 (TrE:
01-DEC-2001 (TrE:
01-DEC-2001 (TrE:
NA H-ANTIPORTOR.
                                                                                                                                                                                       SEQUENCE FROM N.A.

Iida S., Kusumi T., Yonekura-Sakakibara K., Tanaka Y.;

"Plant Na-H antiportor.";

Plant Na-H antiportor.";

Submitted (NOY-2000) to the EMBL/GenBank/DDBJ databases

EMBL; AB051819; BAB56107.1; -.

SEQUENCE 555 AA; 61315 MW; FEF9556E029B3983 CRC64;
                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Lamiales incertae sedis; Toreni
                                                                                                                                                                                                                                                                                            Torenia hybrida.
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                THPURPLE.
                                                                                                                                                                                                                                                         NCBI_TaxID=75807;
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VFGEGVVNDATSVVLFNAVQNFDLPHMSTAKAFELVGNFFYLFATSTVLGVLTGLLSAYI
         VFGEGVVNDATSVVLFNAIQSFDMTSFDPKIGLHFIGNFLYLFLSSTFLGVGIGLLCAYI 238
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                                                                                                                                                             Similarity
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                                                                                                                                                    Conservative
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                                                                                                                                                              70.6%;
70.5%;
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                                                                                                                                                                      Score 1953.5;
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annotation
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                                                                                                                                                                      DB 10; Length
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                                                                                                                                                                                                                              Query Match
Best Local S
Matches 381
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Q9SQU0;
Q1-MAY-2000
Q1-MAY-2000
Q1-DEC-2001
PUTATIVE SOD:
F24P17.16
                                                                                                                                                                                                                                                                                   InterPro; IPR001179; FKBP_PPIASE.
InterPro; IPR000676; NaH_Exchangr.
Pfam; PF00999; NaH_Exchanger; 1.
PRINTS; PR01084; NAHEXCHARR.
PROSITE; PS00453; FKBP_PPIASE_1; UNKNOWN_1.
SEQUENCE 552 AA; 61135 MW; FB4317D8A874FCE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CV. COLUMBIA;
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H.
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC F24P17 ge
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ data
EMBL; AC011623; AAF08577.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID-3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                      121
        180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              536
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                                                                                           CTGVVILLLSGGKSSHLLVFSEDLFFIYLLPPIIFNAGFQVKKKQFFVNFMTIMLFGAIG
                                                                                                                                                                          MAFGLSSLLQNSD-LFTSDHASVVSMNLFVALLCACIVLGHLLEENRWVNESITALIIGL 59
                               TLISFVIISFGAKHLFEKMNIGDLTIADYLAIGAIFSATDSVCTLQVLNQDETPLLYSLV
FGEGVVNDATSVVLFNAIQSFDMTSFDPKIGLHFIGNFLYLFLSSTFLGVGIGLLCAYII
                                                                                                                                                    YVPGSPTERSVR
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(TremBLrel. 13, Last sequence update)
(TremBLrel. 19, Last annotation update)
DIUM PROTON EXCHANGER.
                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           547
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                                                                                                                                                                                                                                           69.6%;
                                                                                                                                                                                                                            59;
                                                                                                                                                                                                                         Score 1925.5; DB 10; Length Pred. No. 2.2e-139; 9; Mismatches 94; Indels
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Q94BM4; PRELIM
Q94BM4;
01-DEC-2001 (Trems)
01-DEC-2001 (Trems)
01-DEC-2001 (Trems)
NA+/H+ ANTIPORTER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
Triticeae; Triticum.
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Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang Z., Zhang J., Chen S.; "Isolation and characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                           FGEGVVNDATSVVLFNAIQNIDINHFDVFVLLQFIGKFLYLFFTSTVLGVAAGLLSAYII
                                                               FGEGVVNDATSVVLFNAIQSFDMTSFDPKIGLHFIGNFLYLFLSSTFLGVGIGLLCAYII
                                                                                                                                TLISCSIISFGAVKIFKHLDIDFLDFGDYLAIGAIFAATDSVCTLQVLSQDETPLLYSLV
                  KKLYFGRHSTDREVALMMLMSYLSYIMAELFYLSGILTVFFCGIVMSHYTWHNVTESSRV
                                                                                                                TLISFVIITFGAMGLFSKLDVGPLELGDYLAIGAIFSATDSVCTLQVLNQDEAPLLYSLV
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                                                                                                                                                                                                                                                                                                            67.4%; Score 1865.5; DB 1 68.2%; Pred. No. 8.7e-135; tive 67; Mismatches 92;
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Last sequence update)
Last annotation update)
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Matches
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Q93YH2;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation updat
NA+/H+ ANTIPORTER, ISOFORM 1.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tomato."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                          VLFNAIQSFDMTSFDPKIGLHFIGNFLYLFLSSTFLGVGIGLLCAYIIKKLYFGRHSTDR
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Spermatophyta; Magnoliophyta; eddicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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